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Perfect score: Sequence: Scoring table:

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Chimeric; Marek's disease virus; outer membrane protein; fusion protein; antigen; vaccine; poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.64
/note= "derived from Marek's disease virus gB protein"
65.456
/note= "derived from M. gallisepticum antigenic protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybrid Marek's disease virus/M. gallisepticum 40 K-S protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Marek's disease gammaherpesvirus.
Chimeric - Mycoplasma gallisepticum.
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                                                                                                                                                                                                AAU34389
AAU37490
AAX58435
AAX69508
AAW89801
                                                                                                                                                                                                                                                                                                                                                                  AAU37374
AAW55640
AAY17187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU37487
AAU37018
                 AAR63226
AAR79910
AAW11978
                                                                                AAP93649
AAR06439
                                                                                                                                                AAU37403
AAG83030
                                                                                                                                                                                                                                                                                                                                 AAR95273
AAU34320
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AAU34412
AAU37520
                                                                 AAR56973
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                                                                                                                                  AAR06438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW36050 standard; Protein; 456 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsuzaki Y, Yanagida N;
 97WO-JP01084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96JP-0103548
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Mycoplasma gallise
Mycoplasma gallise
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M.gallisepticum 26
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1 CMSITKKDANPNNGQTQLEA......SSNENNADKIPGYRRPGTFL
                                                                                                            June 12, 2002, 10:42:12; Search time 55.68 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
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AAR63230
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Gapop 10.0 , Gapext 0.5
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1998 1994 1910 1856 1612 1612 1142 1142 1142

Score

Result No.

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                                                                                                   This sequence represents the chimeric protein 40 K-S which comprises a fragment of the Marek's disease virus outer membrane protein gB fused to an antigenic protein from Mycoplasma gallisepticum. The chimeric protein can be used in recombinant live vaccines for prevention of infection by Mycoplasma gallisepticum, especially as the outer membrane protein shows antigenicity in poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..672 "derived from Marek's disease virus gB protein" 693..1086
                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                               303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGN 360
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS
                                                                                                                                                                                                                                                                                                                                                         STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN
                                                                                                                                                                                                                                                                                                                                                                      181 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE
                                                                                                                                                                                                                                                                                                                                                                                                                  protein comprising herpes virus outer membrane protein and nic polypeptide – for prevention of infection by Mycoplasma
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                     DB 18; Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "derived from M. gallisepticum antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid Marek's disease virus/M. gallisepticum 40 K-C protein
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                  Query Match 100.0%; Score 1998; DB 18; Best Local Similarity 100.0%; Pred. No. 2.1e-126; Matches 393; Conservative 0; Mismatches 0;

    Marek's disease gammaherpesvirus.
    Mycoplasma gallisepticum.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 MNKVAPMIGNIYLSSNENNADKIPGYRRPGTFL 393
                                                                            Disclosure; Page 16-19; 51pp; Japanese
                                                        gallisepticum, especially in poultry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW36051 standard; Protein; 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen; vaccine; poultry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                             polypeptide
WPI; 1997-503046/46.
N-PSDB; AAT96595.
                                                                                                                                                                                   456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998
                                             antiqenic
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Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Region
                                   Fusion
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This sequence represents the chimeric protein 40 K-C which comprises a fragment of the Marek's disease virus outer membrane protein gB fused to an antigenic protein from Mycoplasma gallisepticum. The chimeric protein can be used in recombinant live vaccines for prevention of infection by Mycoplasma gallisepticum, especially as the outer membrane protein shows antigenicity in poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 PSSRILANTNSITDVSWIYSLAGINTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein comprising herpes virus outer membrane protein and antigenic polypeptide – for prevention of infection by Mycoplasma gallisepticum, especially in poultry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1994; DB 18;
Pred. No. 1.2e-125;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 22-30; 51pp; Japanese.
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97WO-JP01084
                                    96JP-0103548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.8
Best Local Similarity 99.7
Matches 392; Conservative
                                                                         (JAPG ) NIPPON ZEON KK
                                                                                                              Tsuzaki Y,
                                                                                                                                                 WPI; 1997-503046/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1086 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                    N-PSDB; AAT96596
                                    29-MAR-1996;
28-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1995
                                                                                                              Saito S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR63230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR63230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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813

240 933

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Gaps

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387 mnkvapmigniylssnennadki 409
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                                                                           AAR63229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                  Saeki S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147
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                                          AAR63229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                             A restriction fragment of the insert of M.gallisepticum genomic clone pUM-67 containing an open reading frame was sequenced (AAG77857). The ORF encodes an antiquent polypeptide (AAR63230). A recombinant avipox virus comprising the coding sequence can be used as a live vaccine to protect against infection by Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide -
the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                           1..615
/note= "Trp residues correspond to TGA codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 615;
                    recombinant avipox virus; live vaccine; mycoplasma antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                              Ohsawa I;
                                                                                                                                                                                                                                                                                                               encoding a
useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1910; DB 15;
Pred. No. 2.5e-120;
3; Mismatches 4;
                                                                                                                                                                                                                                              Ohkawa S,
Mycoplasma gallisepticum antigen (UM-67)
                                                                                                                                                                                                                                                                                                               Recombinant avipox virus combining DNA exhibiting antigenicity of mycoplasma,
                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 87-91; 123pp; Japanese.
                                                               Location/Qualifiers
                                                                                                                                                                                                                                              Iritani Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNKVAPMIGNIYLSSNENNADKI 383
                                                                                                                                                                                                                                                       Takahashi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.6%;
                                                                                                                                                      94WO-JP00541
                                                                                                                                                                           93JP-0074139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                          gallisepticum.
                                                                                                                                                                                                                                             Funato H,
                                                                                                                                                                                                                                                                             WPI; 1994-333181/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 376; Conserv
                                                                                                                                                                                                                                                        Saitos,
                                                                                                                                                                                                                                                                                                                                     of a live vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                 615 AA;
                                                                                                                                                                                                                                                                                        N-PSDB; AAQ77857.
                                                                                                                                                     31-MAR-1994;
                                                                                                                                                                           31-MAR-1993;
30-SEP-1993;
                                                                                                           WO9423019-A
                                                                                                                               13-0CT-1994
                                           Mycoplasma
                                                                                                                                                                                                                                              s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                        Saeki S,
                                                                           Protein
                                                                                                                                                                                                                                               Aoyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327
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A restriction fragment of the insert of M.gallisepticum genomic clone pUM-66 containing an open reading frame was sequenced (AAQ77856). The ORF encodes an antigenic polypeptide (AAR63229), A recombinant avipox virus comprising the coding sequence can be used as a live vaccine to protect against infection by Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nnlnatleglkmaktnlesaingantdkttfdnehpnlveaykalkttlegratnlegls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide -
the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                    codons "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 610;
                                                                                                                                                   recombinant avipox virus; live vaccine; mycoplasma antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                          Location/Qualifiers
1..610
/note= "Trp residues correspond to TGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohsawa I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant avipox virus combining DNA encoding a exhibiting antigenicity of mycoplasma, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1856; DB 15;
Pred. No. 1.1e-116;
); Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.9%; Scur.
95.5%; Pred. No. 1...
... 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohkawa S,
                                                                                                                Mycoplasma gallisepticum antigen (UM-66).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 78-81; 123pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Funato H, Iritani Y,
aitos, Takahashi K;
 610
AAR63229 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                  94WO-JP00541
                                                                                                                                                                                                                                                                                                                                                                                                                      93JP-0074139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI & CO LTD.
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                       Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-333181/41.
N-PSDB; AAQ77856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saitos,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    610 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of a live vaccine
                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-1993;
30-SEP-1993;
                                                                        23-JUN-1995
                                                                                                                                                                                                                                                                                                         WO9423019-A
                                                                                                                                                                                                                                                                                                                                               13-0CT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aoyama S,
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AAR44493

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The plasmid pUTTW-IP contains a sequence (the TTW-I gene) coding for the 40kD antigen of Mycoplasma gallisepticum under the control of a synthetic promoter. A 1300 bp restriction fragment containing the promoter-ORF sequence was excised and was used in the construction of plasmid pNZ7929-R2. This in turn was involved in the construction of a recombinant avipox virus vector comprising the TTW-I gene, DNA encoding the signal membrane anchor peptide from Newcastle Disease Virus haemagglutinin neuraminidase and FPV sequences. The recombinant avipox virus is useful as a live vaccine
                                                                                                                                    PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 300
                                                                                                                                                    nnlnatleq1kmaktnlesainqantdkttfdnehpnlveaykalkttlegratnlegla 146
                         Recombinant avipox virus combining DNA encoding a polypeptide - exhibiting antigenicity of mycoplasma, useful for the production of a live vaccine
                                                                                                                                                                                                                                                                                                                                                                                                    recombinant avipox virus; live vaccine; mycoplasma 40kD antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohsawa I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "corresponds to a NNN codon'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "corresponds to a NNN codon"
                                                                                                                                                                                                          301 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohkawa S,
                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma gallisepticum 40kD antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 71-74; 123pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ney
Misc-difference 262
                                                                                                                                                                                                                                                                                          Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takahashi K;
                                                                                                                                                                                                                                                                                         AAR63227 standard; Protein; 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93JP-0074139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-JP00541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                 23-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma gallisepticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI & CO I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-333181/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saitos,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ77854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9423019-A
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                                                                                                                                                                                                                                                                                                                     AAR63227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aoyama
                                                                                                                                           241
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                                                                                     181
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                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 300
                                                                        The sequence coding for the 40kDa antigen was obtained by PCR amplification of Mallisepticum genomic DNA. The antigen reacts with Mycoplasma-immune or Mycoplasma-infected serum and can be used as a vaccine to protect fowl from M.gallisepticum infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "corresponds to NNN codon in AAQ53419"
                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "corresponds to NNN codon in AAQ53419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma gallisepticum antigen and DNA coding for it for vaccination of fowl against mycoplasma infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1612; DB 14;
Pred. No. 1.4e-100;
; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ś
                                                                                                                                                                                                                                                                                                                                        Vaccine; mycoplasma infection; poultry; fowl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohkawa
                                                                                                                                                                                                                                                                                                           Mycoplasma gallisepticum 40kD antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          claim 2; Page 23-26; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aoyama S, Fujisawa A, Iritani Y,
                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                             AAR44493 standard; Protein; 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                             MNKVAPMIGNIYLSSNENNADK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.7%;
illarity 95.0%;
Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93WO-JP00715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92JP-0138819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma gallisepticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JAPG ) NIPPON ZEON KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-405837/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                        283
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                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Sim
nes 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9324646-A
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                                                                                                                                                                                                                   AAQ94711 encodes AAR76955 Mycoplasma gallisepticum antigenic protein TTM-1. TTM-1 can be used as a vaccine for M. gallisepticum infectious diseases in poultry, and as a diagnostic agent for
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an
                                                                                                                                                                                                                                                                    1 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                                                   241 PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Mycoplasma gallisepticum (MG1) polypeptide.
                                                                                                                                                                                                                                                          STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN
                                                                                                                                                                                                                                                                                                           ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aoyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This amino acid sequence of MG1 is encoded by M1 DNA and elicits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as
                                                                                                  Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iritani Y,
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Mycoplasma gallisepticum
                                                                                                  80.3%; Score 1604; DB 16;
llarity 94.4%; Pred. No. 4.7e-100;
Conservative 7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                            301 YKLNNGNVOQVEFATSTSANNTTANPTPAVDEIKVAK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma gallisepticum; Poultry vaccine; ss;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NIPPON ZEON KK.
) SHIONOGI SEIYAKU KABUSHIKI KAISHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig.1a; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yanagida N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP93646 standard; protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89EP-0005441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88JP-0136343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma gallisepticum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-358393/49.
                                                                                                   Ouery Match
Best Local Similarity
Matches 318; Conserv
                                                              368 AA;
                                   M. gallisepticum.
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AAP93646
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                                                                                                                                                                              STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
                                                                                                                                                                                                                                ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 240
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                             A new antigenic protein which reacts with Mycoplasma gallisepticum is useful in a component vaccine for use against poultry infected with M. gallisepticum.
                                                                                      ;
0
                                                              Length 368;
to protect against infection by Mycoplasma gallisepticum.
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigenic protein; vaccine; poultry; diagnosis; TTM-1.
                                                           Score 1612; DB 15;
Pred. No. 1.4e-100;
6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma gallisepticum antigenic protein TTM-1
                                                                                                                                                                                                                                                                                                                                                                                    YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "any amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR76955 standard; Protein; 368
                                                             80.7%;
95.0%;
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                                                                                     Conservative
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N-PSDB; AAQ94711.
                                                                         Similarity
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                                                           Query Match
Best Local Simi
Matches 320;
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                         Sequence
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NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                              STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
           CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                      Mycoplasma gallisepticum; poultry; vaccine.
                                                                                                                                                                                                                   protein; 261
                                                                                                                                                                                                                                                                                                                                                                                           89JP-0136343.
                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                (JAPG ) NIPPON ZEON KK.
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                                                                                                                                                                                                                  AAR05082 standard;
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les 228; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ04687
                                                                                                                                                                                                                                                                                  TMG-1 antigen.
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antigen-antibody reaction with anti-MG poultry sera. It can be used as a vaccine to prevent and diagnose MG infection. Doseage is at least 1 micro gram vaccine / kg. No acute toxicity was noted with a dose of 5 mg / kg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding the protein can be inserted into an expression vector for the prodn. of MG-1 polypeptide which elicits an antigen-antibody reaction with anti-mycoplasma gallisepticum poultry sera. It may also be ligated to other DNA to produce fusion proteins with an N-terminal bacterial enzyme sequence.
                                                                                                                                                                                                                    61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                                                                                         121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
                                                                                                                               1 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                                                                                                                                                                                                                                                    181 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 235
                                                                                                                                                                                                                                                              Diagnostic and vaccine for poultry mycoplasma serum - utilises antigen protein of the disease and recombinant vector incorporated with its coding gene.
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                                                                         Length
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.2%; Score 1142; DB 11; Best Local Similarity 97.0%; Pred. No. 2.9e-69; Matches 228; Conservative 3; Mismatches 4;
                                                                        Score 1142; DB 10;
Pred. No. 2.9e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma gallisepticum; poultry; vaccine.
                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See also AAR05081-2 and AAR06437-41.
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                                                                                                                                                                                                                                                                                                                             235
                                                                         57.2%;
97.0%;
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                              Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI KK.
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N-PSDB; AAQ04686.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           MG-1 antigen
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DNA encoding the protein can be inserted into an expression vector for the prodn. of MG-1 polypeptide which elicits an antigen-antibody reaction with anti-mycoplasma gallisepticum poultry sera. It may also be ligated to other DNA to produce fusion proteins with an N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 cmsitkkdanpnngqtq1qaarmeltdlinakartlas1qdyakieas1ssayseaetvn 86
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Diagnostic and vaccine for poultry mycoplasma serum - utilises antigen protein of the disease and recombinant vector incorporated with its coding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.2%; Score 1142; DB 11; Length 261; 97.0%; Pred. No. 3.4e-69; Live 3; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                   bacterial enzyme sequence.
See also AAR05081 and AAR06437-41.
                                                                                                                                                 Claim 2; Fig 2; 20pp; Japanese.
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Indels

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AAR79911;

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This AA sequence of TMG-1 is encoded by TM-1 base sequence. It has the same sequence as that of a polypeptide expressed in Mycoplasma gallisepticum in nature. When the corresponding DNA sequence is inserted 'into a recombinant vector used to transform a host the antigen protein produced can be used as a vaccine to prevent and diagnose MG infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINE-QKT 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antigenic proteins of Mycoplasma gallisepticum - useful as
                  181 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yanagida N, Kamogawa K, Iritani Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1117; DB 10
                                                                                                                                                                                                                                                            Mycoplasma gallisepticum; Poultry vaccine; ss;
                                                                                                                                                                                                                           Amino acid (AA) sequence of TMG-1 polypeptide.
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3; Mismatches
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                                                                                                                      AAP93959 standard; protein; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.9%;
96.2%;
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                                                                                                                                                                                           (first entry)
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Best Local Similarity 96.2
Matches 227; Conservative
                                                                                                                                                                                                                                                                                                 Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saito S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-358393/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 AA;
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                                                                                                      AAP93959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence of a 261 amino acid protein encoded by a fragment of the Mycoplasma gallisepticum genome. The encoding sequence and the sequence of AAT04075 (encoding a 661 amino acid protein) can be used to detect M.gallisepticum using probes based on nucleotides 1125-1648 and primers based on nucleotides 449-466, the complement of bases 893-919, 1908-1934 and the complement of bases 2184-2210 of AAT04075 and a probe based on nucleotides 718-41 of the DNA encoding this protein. The method using these sequences is faster i.e. is able to detect M.gallisepticum, which causes avian chronic respiratory diseases, within one day, from avian secretions, washings from the lung, respiratory tract, nasal cavity, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection; probe; primer; PCR; amplification; secretion; lung; avian chronic respiratory disease; respiratory tract; nasal cavity.
                                                                  Detection of Mycoplasma gallisepticum - for the quick detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 261;
                                                  ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i.e. within one day, of avian chronic respiratory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 3.4e-69;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1142;
                                                                                                                                                                                                                                                                              M.gallisepticum 261 amino acid protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 10-11; 11pp; Japanese.
                                                                                                                                                                           Ą
                                                                                                                                                                       AAR79911 standard; Protein; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.2%;
97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94JP-0052764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94JP-0052764
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JAPG ) NIPPON ZEON KK (SHIO ) SHIONOGI & CO )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-347462/45.
N-PSDB; AAT04076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   JP07236498-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1994;
                                                                                                                                                                                                                                           19-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Simi
Matches 228;
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Aoyama

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Gaps 9 86

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Indels

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Sequence

Query Match

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27

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Length 261;

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343 --nvglqyklnggdtkqinfvqtpasgssdvaaneeetmaspaemqsaptvddikiakva 400
                                                                                                                                                                                                                                                                                                                       Detection; probe; primer; PCR; amplification; secretion; lung; avian chronic respiratory disease; respiratory tract; nasal cavity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of Mycoplasma gallisepticum – for the quick detection, i.e. within one day, of avian chronic respiratory diseases
                                340 LSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "encoded by TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "encoded by TGA"
                                                                                                                                                                                                                                                                                           M.gallisepticum 661 amino acid protein.
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "encoded by
                                                                                                                                                                                                  AAR79910 standard; Protein; 661 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note- "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94JP-0052764.
                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JAPG ) NIPPON ZEON KK.
                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 42.8
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                         380 ----ADKIPGY 386
                                                                                                                        456 ptavtvdllkgy 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-347462/45.
N-PSDB; AAT04075.
                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 220
                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP07236498-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1994;
                                                                                                                                                                                                                                                             19-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-1995.
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                                                                                                                                                                                                                                  AAR79910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A restriction fragment of the insert of M.gallisepticum genomic clone pUM-81 containing an open reading frame was sequenced (AAQ77853). The ORF encodes an antigenic polypeptide (AAR63226). A recombinant avipox virus comprising the coding sequence can be used as a live vaccine to protect against infection by Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANNVGLQYKLNNGNVQQVEF-----ATSTSAN--NTTANP-----TPAVDEIKVAKIV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 -----PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYG-PSTGYLYFPYKLVKAAD 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 DANPNNGQTQLEAARMELTD-----LINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant avipox virus combining DNA encoding a polypeptide exhibiting antigenicity of mycoplasma, useful for the production of a live vaccine
                                                                                                                                                   Location/Qualifiers
1..661
/note= "Trp residues correspond to TGA codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.3%; Score 806; DB 15; Length 661;
42.8%; Pred. No. 4.4e-46;
live 62; Mismatches 123; Indels 65
                                                                                         recombinant avipox virus; live vaccine; mycoplasma antigen.
                                                                                                                                                                                                                                                                                                                                                                                                  Ohsawa I;
                                                                                                                                                                                                                                                                                                                                                                                                  Ohkawa S,
                                                           Mycoplasma gallisepticum antigen (UM-81).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 61-65; 123pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                  Funato H, Iritani Y,
                                                                                                                                                                                                                                                                                                                                                                                                               Saitos, Takahashi K;
                                                                                                                                                                                                                                                                                                                       93JP-0245625.
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                            (first entry)
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                                                                                                                        Mycoplasma gallisepticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                     JAPG ) NIPPON ZEON KK.
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N-PSDB; AAQ77853.
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Best Local Similarity
Matches 185; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199
                                                                                                                                                                                                                                                                           31-MAR-1994;
                                                                                                                                                                                                                                                                                                        31-MAR-1993;
                                                                                                                                                                                                                                                                                                                        30-SEP-1993;
                            23-JUN-1995
                                                                                                                                                                                                                WO9423019-A
                                                                                                                                                                                                                                              13-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                  Aoyama S,
AAR63226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Saeki S,
                                                                                                                                                                     Protein
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12;
                                                                This is the amino acid sequence of a 661 amino acid protein encoded by a fragment of the Mycoplasma gallisepticum genome. The encoding sequence and the sequence of AAT04076 (encoding a 261 amino acid protein) can be used to detect M.gallisepticum using probes based on nucleotides 1125-1648 and primers based on nucleotides 449-466, the complement of bases 893-919, 1908-1934 and the complement of bases 2184-2210 of the sequence, and a probe based on nucleotides 718-41 of AAT04076. The method using these sequences is faster i.e. is able to detect M.gallisepticum, which causes avian chronic respiratory diseases, within one day, from avian secretions, washings from the lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.3%; Score 806; DB 16;
42.8%; Pred. No. 4.4e-46;
tive 62; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               respiratory tract, nasal cavity, etc.
Claim 2; Page 7-10; 11pp; Japanese.
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Search completed: June 12, 2002, 10:48:38 Job time: 386 sec
                                                                                                                           Query Match
Best Local Simi
Matches 169;
                                                                                                     Sequence
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                                                                   NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                    ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 240
                                                                                                             ANNVGLQYKLNNGNVQQVEF-----ATSTSAN--NTTANP-----TPAVDEIKVAKIV 339
                                                                                                                                                                             340 LSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSS-------NENN 379
                                                                                                                                                                                                           DANPNNGQTQLEAARMELTD-----LINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                    ----PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYG-PSTGYLYFPYKLVKAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New promoter region from a Mycoplasma gallisepticum adhesin gene useful when coupled to foreign antigen gene, for prodn. of
                                                                                                                                                                                                                                                                                                                                                                                                     1.25
/label= Sig_peptide
/note= "the signal peptide shows homology to
the pMGAl.3 signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whithear KG;
                                                                                                                                                                                                                                                                                                                                                       Adhesin; pMGA; mycoplasma; dlagnosis; vaccine; vector; respiratory disease; poultry; haemagglutinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Walker ID,
                                                                                                                                                                                                                                                                                                                                         Mycobacterium gallisepticum pMGA1.2 adhesin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Markham PF,
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                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma gallisepticum strain S6.
                                                                                                                                                                                                                                                                                         AAW11978 standard; Protein; 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94CA-2135330.
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                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glew MD,
                                                                                                                                                                                                                                   -----ADKIPGY 386
                                                                                                                                                                                                                                               ptavtvdllkgy 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BROW/) BROWNING G F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-241027/32.
N-PSDB; AAT51531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Browning GF,
                                                                                                                                                                                                                                                                                                                         23-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-1994;
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10-NOV-1993;
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Peptide
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61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 DANPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
multivalent live vaccines, also new probes for detecting Mycoplasma and manipulating its genome
                                                                                                                         Adhesin pWGA1.2 (AAW11978) and adhesin pMGA1.3 fragment (AAW11979) are products of gene sequences (see also AAF15131) isolated from Mycoplasma gallisepticum. DNA constructs incorporating the promoter and/or signal sequences of the pWGA genes can be used in the produ. of multivalent live vaccines. The signal peptide sequence is utilised where attachment of an exogenous antigen gene to the mycoplasma cell membrane is required.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enatkladsllssivkkitgvee-----ahnkaqpanysfygykrwytellldkqvfp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYKYARRTVW-NGDEPSSRILANT-----NSITDVSWIYSLAGTNTKYQFSFSNYGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 TN----ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV----
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 IKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                1 35.7%; Score 713; DB 16; Similarity 41.1%; Pred. No. 7.7e-40; 59; Conservative 60; Mismatches 124;
                                                                              Disclosure; Fig 3; 81pp; English.
                                                                                                                                                                                                                                                                                                                                       647 AA;
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GenCore version 4.5
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OM protein - protein search, using sw model

June 12, 2002, 10:46:22 ; Search time 29.99 Seconds (without alignments) 1259.190 Million cell updates/sec Run on:

US-09-147-052-2\_COPY\_64\_456 1998 1 CMSITKKDANPNNGQTQLEA......SSNENNADKIPGYRRPGTFL 393 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	major surface prot	major surface prot	major surface prot	major surface prot	hemagglutinin homo	major surface prot	major surface prot	hypothetical prote	surface-located me	hypothetical prote	FmtB protein [impo	hypothetical prote	fibrinogen-binding	hypothetical prote		hypothetical prote	subtilisin-like pr	1mp1 protein - Myc	ble oute	surface membrane p	<pre>lmp1 protein - Myc</pre>	toxin-like outer m	probable autotrans	ser-lys rich hypot	hemagglutinin homo	probable invasin Z	phage-related prot	_	hypothetical prote
SOMESTES	ΙD	S48754	S48753	S48751	S48752	A49218	S48755	S51560	B89921	JC6009	AG2422	D90011	C89921	S41539	B71605	A86827	F82885	S44131	T30822	D71850	PC6003	T18351	H71879	AC0976	T40462	B49218	E85822	F96907	D71917	AG2560
	DB C	7	7	7	2	2	2	7	3	7	7	1 2	7	3	7	7	7	7	2	7	7	1 2	6	7	1 2	2	0	2	7	7 2
,	Length DB	702	70.	650	64	647	386	35(	6713	130	661	2481	3890	933	.08	107	468	683	1365	1237	624	1051	2399	1107	75.	135	266	1645	3194	1487
* 6.0	_ '	41.6	37.7	37.2	37.2	35.7	28.8	9.5	8.8	8.7	8.3	8.2	8.2	8.0	7.8	7.8	7.8	7.7	7.7	7.6	7.6	7.5	7.3	7.2	7.2	7.1	7.1	7.1	7.0	7.0
	Score	831.5	754	744	743	713	575.5	189.5	175	173	165.5	164.5	163.5	159	156	155	155	154.5	154.5	151.5	151	150.5	145	***	143.5	142	142	•	140.5	139.5
+[	No.	7	7	e	4	'n	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58

rhoptry protein - transcription requ	cell surface antig	conserved hypothet	fibrinogen-binding	surface layer prot	filamentous hemagg	hypothetical prote	membrane associate	kinesin-related pr	hypothetical prote	hypothetical prote	kinesin-like prote	hypothetical prote	rhoptry protein -	hypothetical prote
T28676 TNBYR6	T17519	AE1130	D89852	S68553	T31102	S55119	E97066	S14032	F90073	F82884	T38378	A64596	T28677	B97806
77	7	7	~	~	~	~	7	~	7	7	~	7	~	7
2401	820	926	686	1524	4152	719	568	1073	2271	5005	1085	1238	2269	589
0.7	6.9	6.9	6.9	6.9	6.9	6.9	9.8	6.8	8.9	6.8	6.8	8.9	6.8	6.7
139.5	37.5	137.5	137.5	137.5	137.5	137	136.5	136.5	136.5	136	135.5	135.5	135	134.5
13	П	-												

# ALIGNMENTS

	RESULT 1 S48754 major surfamajor surfamajor surfamajor C; Species: C; Date: Ol-C; Accession R; Martle: ThA; Title: ThA; Title: ThA; Refection A; Residuals: p A; Residuals: p A; Residuals: A; Cross-ref; C; Genetics: A; Canetics: A; Start cod A; Start co	RESULT 1 S48754 Major surface protein (clone pMGA1.4) precursor - Mycoplasma gallisepticum major surface protein (clone pMGA1.4) precursor - Mycoplasma gallisepticum C: Species: Mycoplasma gallisepticum C: Mycopl
· · · · · · · · · · · · · · · · · · ·	Query N Best L Matches	Query Match Best Local Similarity 42.0%; Pred. No. 3.2e-38; Matches 173; Conservative 84; Mismatches 116; Indels 39; Gaps 8;
	99 qa	8 DANPINGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNN 61 :
	Qy 62 Db 128	62 NLNATLEQLKMAKTNILESAINQANTDKTTFDNEHPNIJVEAYKALKTTLEQRATNILEGLSS 121   :      :    :  :  :   :
	Qy 122 Db 188	2 TAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNA 181 : :
	Oy 182 Db 247	182 DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 235 
	Oy 236	236 WNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVK 290 
	Qy 291 Db 366	291 AADANNVGLOYKLNNGNVOQVEFATSTSANNTTANPTPAVD 331 :: ::  :       :::   366 SSDSDKVALEYKLNESAVKTIDFSPSQTSPVASDATRENNRSTAAPAQGSTEINPAPTLD 425
	Qy 332 Db 426	332 EIKVAKIVLSGLRFGONTIELSVP-TGEGNMNKVAPMIGNIYLSSNENNADK 382 

40;

Length 650;

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A;Cross-references: GB:U90714; EMBL:L28423; NID:g1905869; PIDN:AAB50152.1; PID:g19058 R;Markham, P.F.; Glew, M.D.; Brandon, M.R.; Walker, I.D.; Whithear, K.G. Infect. Immun. 60, 3885-3891, 1992 A;Title: Characterization of a major hemagglutinin protein from Mycoplasma gallisepti A;Reference number: A44793; MUID:92363591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 FPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTAN-PTPAVDEIKVAKIVLSG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL:-STINEQKTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTVW-NGDEPSSRILANT-----NSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 NPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.2%; Score 743; DB 2; Length 64
42.3%; Pred. No. 2e-33;
ive 62; Mismatches 125; Indels
                                                                                                                                                                                                                                                                 A;Note: sequence extracted from NCBI backbone (NCBIP:111017) C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 LRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 744; DB 2;
Pred. No. 1.8e-33;
2; Mismatches 127
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42.9%; Pred
tive 62; 1
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Best Local Similarity 42.3
Matches 172; Conservative
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                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 26-42 < MA2>
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Best Local Similarity
Matches 172; Conserv
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A; Start codon: GTG
                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                 A;Genetic code: SGC3
A;Start codon: GTG
                                                                                                                                                  A; Accession: A44793
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                                                                                             Sacrata surface protein (clone pMGAL.3) precursor - Mycoplasma gallisepticum C. Species: Ol-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999  
C. Ancession: S48753  
R. Markham, P.F.; Glew, M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F.; FEBS Lett. 352, 347-352, 1994  
R. Marcham, P.F.; Glew, M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F.; FEBS Lett. 352, 347-352, 1994  
R. Reference number: S48751  
MulD:95010739  
R. Secession: S48753  
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTP----VNYKYARRTVW 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGD--EPSSRILANTN-SITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAAD 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYN 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.7%; Score 754; DB 2; I 41.6%; Pred. No. 5.6e-34; Live 62; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 41.6
Matches 176; Conservative
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283

438

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major surface protein (clone pMGA1.2) precursor - Mycoplasma gallisepticum C; Species: Mycoplasma gallisepticum C; Species: Mycoplasma gallisepticum C; Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999 C; Accession: S48752 R; Markham, P.F.; Glew, M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F. A; Title: The organisation of the multigene family which encodes the major cell surface A; Reference number: S48751; MUID:95010739
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross references: EMBL: L28424; NID: 9535687; PIDN: AAA62416.1; PID: 9535689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 649;
                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-649 <MAR>
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1;

Gaps

48;

QY 8 DANDNINGOTOLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSBAETVN 60	NVQQVEFATSTSANNTTANPTPAV
40 DINFOUSQUERRANDS ELAMANMOLITIFUS NANNOLIYUI ANIQNILINA I DAANIYL	Db 338 SIGYLYFPYKI,VNTSDQVKLGLEYKLNDATKPSAITFGSDQTMNGKTPTVND 389
Qy 61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEGRATNLEGLS 120 	333 IKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI
QY 121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQK 178 	EKVSPMIGNMY LSSSPNNWNKI 43
<pre>Qy 179 THADALSHSFIKKVIQNNEQSFVGTFTHANVQPSNYSFVAFSADVTPVNYKY 230</pre>	848755 major surface protein (clone pMGA1.5) precursor - Mycoplasma gallisepticum (fragment) C. Species: Mycoplasma gallisepticum C. Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999
QY 231 ARRTVW-NGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGY 281	C. Accession: S48755 R. Markham, P.F.; Glew, M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F. FEBS Lett. 352, 347-352, 1994 A. Title: The organisation of the multigene family which encodes the major cell surfac
Qy 282 LYFPYKLVRAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVA 336	A; Marerence number: 548/31; Mull:93010/39 A; Accession: 548/31; nucleic acid sequence not shown A; Molecule type: DNA
QY 337 KIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 383  :  :  :	A; Residues: 1.386 < NAR> A; Cross-references: EMBL:L28424; NID:g535687; PIDN:AAA62419.1; PID:g535692 A; Cross-references of residues 385-386 and the corresponding nucleotide sequence ar C; Genetics: A; Genetic code: SGC3
nemaystutinin homozog prost. – mycopiasma yaitisepticum C;Species: Mycopiasma gallisepticum C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 07-Dec-1999 C:Accession: A49218	Length 300; Indels 25; Gaps 10;
R.Markham, P.F.; Glew, M.D.; Whithear, K.G.; Walker, I.D. Infect. Immun. 61, 903-909, 1993 A.Title: Molecular cloning of a member of the gene family that encodes pMGA, a hemagglut	OY 8 DANDNINGOTOLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNN 61 :
A.Accession: A49218 A.Status: preliminary A.Molecule type: DNA: protein	QY 62 NLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSS 121 
A/KOSIGUES: 1-74/ CMAPA	OY 122 TA-YNOIRNNLVDLYNKASSLITKTLDPLN-GGTLLDSNEITTANKNINNTLSTINEQ 177 :
Cydenetics: A;Genetic code: SGC3	QY 178 KTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNY 228
Query Ma Best Loc Matches	QY 229 KYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPS-TGYLYFPYK 287 : :    :    :
<pre>Qy 8 DANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60</pre>	288
OY 61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAVKALKTTLEQRATNLEGLS 120 :  ::  :	DD 301 LVQINDNVGLQIVLNNIIFYLVNF 304 RESULT 7
QY 121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINTLSTINEGK 178  1	S3.1350 R35.1350 R37.1350 R37.
QY 179 TNADALSNSFIKKVIQNNEQSFVGTETNANVQPSNYSFVAFSADVTPV 226 t	
OY 227 NYKYARRTWW-NGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGP 277 	A; Kererene number: 548/31; MulD:930L0/39 A; Accession: 551560 A; Status: nucleic acid sequence not shown A; Molecule type: DNA

sys

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| : | : | | 886 LQGAINDKDATLRNQNYLDADES
                       -----KVAPMIGNIYLSSNEN
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Matches 94; Conserv
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A; Genetic code: SGC3
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hypochetical protein ebhA [imported] - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-0ct-2001
C;Accession: B89921
R;Kuroda, M; Ohtta, T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L; Oguc
Ma, A; Mizutani-Ui, Y; Kobayashi, N; Sawano, T; Inoue, R; Kaito, C; Sekimizu, K;
C; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K.
A;Tille: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Residues: 1-6713 <KUR>
A;Resizersreferences: GB:BA000018; PID:g13701232; PIDN:BAB42527.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 QFSFSNYGPSTGYLYFPYKLVKAADA------NNVGLQYKLN------NGNVQ 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GTNTKY 268
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                                                                                                                                                                                                                                                                                                                                                                                                             291 AADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTI 350
                                                                      PID:9535688
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                                                                                                                                                                                                                                                                 Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6713;
A;Residues: 1-320 <MAR>
A;Cross-references: EMBL:L28424; NID:9535687; PIDN:AAA62415.1;
C;Genetics:
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                                                                                                                                                                                                                                                             ; Score 189.5; DB 2;
; Pred. No. 0.0015;
11; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 ELSVP-TGEGNMNKVAPMIGNIYLSSNENNADKI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.58;
                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 48.9%
Matches 46; Conservative
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                                                                                                                                                           A; Genetic code: SGC3
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A.; Irigu
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hypothetical protein all4935 [imported] - Anabaena sp. (strain PCC 7120)
c) species: Anabaena sp.
A.Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 3,
c) Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C;Accession: AG2422
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.
      C; Species: Mycoplasma hominis
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Accession: JC6009
R; Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G.
J. Bacteriol. 176. 2775-2784, 1996
A; Title: Analysis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp A; Reference number: JC6009; MuID:96213016
                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-1302 <LAD>
A;Cross-references: EMBL:X95601; NID:g1197335; PIDN:CAA64858.1; PID:g1197336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Keywords: duplication; membrane protein
F. 1-24/Domain: signal sequence *status predicted <SIG>
F. 25-1302/Product: surface-located membrane protein Lmp3 *status predicted
F. 25-1302/Domain: tetratricopeptide repeat homology <TT1>
F. 993-1026/Domain: tetratricopeptide repeat homology <TT2>
F. 1089-1120/Domain: tetratricopeptide repeat homology <TT3>
F. 1154-1190/Domain: tetratricopeptide repeat homology <TT3>
F. 1154-1190/Domain: tetratricopeptide repeat homology <TT3>
F. 1154-1190/Domain: tetratricopeptide repeat homology <TT4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 NNNLNATLEQLKMAKTNLESAINQANTDKTTFDN-----EHPN------LVEAYKAL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 FSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;
surface-located membrane protein Imp3 precursor - Mycoplasma hominis
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22.8%; Pred. No. 0.079;
Live 67; Mismatches 163; Indels B
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hypothetical protein ebbB [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
C;Accession: C89921
R;Kuroda, M.; Obta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; (ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, E.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
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A; Reference number: A89758; MUID:21311952; PMID:11418146
A; Recession: C89921
A; Resticus: preliminary
A; Molecule type: DNA
A; Residues: 1-3890 < KUR>
A; Cross-references: GB:BA000018; PID:g13701233; PIDN:BAB42528.1; GSPDB:GN00149
A; Experimental source: strain N315
C; Genetics:
A; Genetics:
A; Genetics:
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                                                                               186 DQAKTTGETSIDQVTPTVNKKATARNEITAILNNKLQEIQATPDATDEEKQAADA--EAN 1243
                                                                                                                                           58 TVNNNLN-----ATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTL-- 109
                                                                                                                                                                                                                                                                 110 -EQRATNLEGLS-----STAYNQIRNNL------VDLYNKASSLITKTLDPLNGGTLL 155
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                      DANPINICOTOLE-----AARMELTDLINAKAMTLASLODYAKIEASLSSAYSEAE
                                                                                                                                                                                                                                                                                                                          1303 NDQNATNEEKEAAIQQLATAVTDAKNNITAATDDNGVDTAKDAGKNSIQSTQP---ATAV
                                                                                                                                                                                                                                                                                                                                                                                      156 DSN-----EITTANKNINNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTFTNAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1542 EKGND 1546
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001.
Affilte: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Tucawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
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Lancet 357, 1225-1240, 2001
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A;Molecule type: DNA
A;Residues: 1-2481 <KUR>
A;Cross-references: GB:BA000018; PID:g13701961; PIDN:BAB43253.1; GSPDB:GN00149
A;Experimental source: strain N315
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                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-661 <KUR>
A;Residues: 1-661 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76634.1; PID:g17134073; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
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A;Reference number: A89758; MUID:21311952; PMID:11418146
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C;Species: Staphylococcus aureus
C;Spate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEOKTNADALSNSFI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKVIQ---NNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDEPSSRIL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 LKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIRN 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.3%; Score 165.5; DB 2; 22.7%; Pred. No. 0.082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 NFNN--ASSRRNTAEQARNQVREETRL 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88;
                                                                                                                                                                                                                                                                                                                                                             A; Gene: all4935
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C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: B71605
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.; Schence 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743
A;Accession: B71605
A;Accession: B71606
A;Accessio
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A86827
A86827
APPROACTED Protein yqfG [imported] - Lactococcus lactis subsp. lactis (strain IL140 bypothetical protein yqfG [imported] - Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: A86827
B;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Accession: A86625; MUID:21235186; PMID:11337471
A;Accession: A86625
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1072 (STC)
A;Cross references: GB:AE005176; PID:912724625; PIDN:AAK05715.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||:: | |||| | :: | |||| | 468 INNNISYT--QLKMNNNINFNINFNIHMESPINQQHNNTFKVNNDTNFFNEPTNKMKKKNKEKK 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               575 QKKHNKMSQVSKQSNNKNNKNNSHLKKQININ------TNNNMDNKNNSHISKNVIVD 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            687 VNNMNNPWYFPNVNIQ-KDDSNIALLYNNKPNIDFNNFQLNHINNHMIQNNIMTNNVMLN 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 VNNNLNATLEQLKMAKT----NLESAINQA--NTDK----TTFDNEHPNLVEAYKALKT 107
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21.0%; Pred. No. 0.59;
tive 76; Mismatches 154; Indels 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.8%;
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Best Local Similarity 21.0%
Matches 97; Conservative
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Best Local Similarity 23.8%
Matches 73; Conservative
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A;Gene: yqfG
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N.Alternate names: clumping factor
C.Species: Staphylococcus aureus
C.Species: Stabylococcus
R.McDevitt, D.; Francois, P.; Vaudaux, P.; Foster, T.J.
Mol. Microbiol. 11, 237-248, 1994
A.Title: Molecular characterization of the clumping factor (fibrinogen receptor) of Staphylococcus number: Stabs MUID: 94224142
A.Reference number: Stabs MUID: 94224142
A.Status: preliminary
A.Status: preliminary
A.Status: 1-933 <MCD>
A.Status: DNA
A.Residues: 1-933 <MCD>
A.Cross-references: EMBL: 218852; NID: 9397525; PIDN: CAA79304.1; PID: 9397526
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                                                                                                                                                                                                                                     KAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDE-IKVAKIVL---SGLRF 345
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hypothetical protein PFB0850c - malaria parasite (Plasmodium falciparum)
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                                                                                             241 -PSSRILLANT-NSITD-----VSWIYS---LAGINTKYQFSFSNYGPSTGYLYFPYKLV
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ESNSVSDQTSSEAS-TNSNSSISLSPSNISSTSDSESATNSSDFSNVAEVANNSLASV 486	-NATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATN 115	ADNLGINQSGSDNLTKDSSEISTSGAFLSSNQTSSEASTNSNSSISL 546	-LSSTAYNOIRNNLVDLYNKASSLITKTLDPLNGG 152	547 SPSNISSTSVLESTTSSSNFSNVAEVANNSLASVNNSSSSVLSSTSTADNLEINQFGSDN 606	153 TLLDSNEITTANKNINNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPS 212	AFLSSNQTSSEASSNSMSSINSPSLSLSLTSNSESAT 655	NYSFVAFSADVIPVNYKYARRIVWNGDEPSSRILANTNSITDVSWIYSLAG 263	NQSNSSEATKVDNNSSTHSSNILNSGSNDSSDSDSDSDSDSSNLSSSPN 704	TNIKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNT- 322	LETNOTISSENPKKVSSSNSVQENSTD 740	TANPTPAVDELSVPTGEG 359	HEMSTNPKSSISSPISTISSSQQKESQSNLLNTTEGINNPITFNNSSSENSAASILISYS 800	360 NMNKVAPMIGNIYLSSNENNADKI 383	NNNSESSETGCLYISNEAQRDNGSEISHSLPSSNSNENNVSSI 843
ESNSVSDQTSSEAS-TNSNSSISL	-NATLEQLKMAKTNLESAINQANT	NNSSSSVLSSTSTADNLGINQSGS	EEG-LSSTAYNOI-	SPSNISSTSVLESTTSSSNFSNVA	TLLDSNEITTANKNINNTLSTINE	LTKDSSEISTSGAFLSS	NYSFVAFSADVTPVNYKYARRTVW	NQSNSSEATKVDN	TNTKYQFSFSNYGPSTGYLYFPYK	LETNOTIS	TANPTPAVDE	HEMSTNPKSSISSPISTISSSQQK	NMNKVAPMIGNIYLS	NNNSESSETGCLYISNEAQRDNGS
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Sednence:

Title:

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APPLICANT: Sacki, Sakiko
APPLICANT: Obsava, Ikuroh
APPLICANT: Funato, Hirono
APPLICANT: Funato, Hirono
APPLICANT: Iritani, Yoshikazu
APPLICANT: Takanshi, Kiyoohito
APPLICANT: Takanshi, Kiyoohito
TITLE OF INVENTION: FOLYPEPTIDE, DNA ENCODING THE
APPLICANT: TORANSHION: POLYPEPTIDE, DNA ENCODING THE
TITLE OF INVENTION: POLYPEPTIDE, DNA ENCOMBINANT VECTOR AS WELL
TITLE OF INVENTION: AS USE THEREOF
UNUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: NAGGHTON, WESTERMAN, HATTORI, MCLELAND &
                          Sequence 28, Sequence 24, A Sequence 2, A Sequence 2, A Sequence 47, Sequence 47, Sequence 15, Sequence 47, A Sequence 47, A Sequence 47, A Sequence 33, A Sequence 33, A Sequence 33, A Sequence 9, A
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COUNTRY: USA
ZIP: 20006
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
OPERATURG SYSTEM: PC-DOS/MS-DOS
OPERATURG SYSTEM: DATA:
                       US-09-268-347-28
US-09-268-347-34
US-08-242-932-2
US-08-144-481-2
US-09-268-347-49
US-09-268-347-49
US-09-38-347-47
US-08-169-37-2
US-09-336-447A-15
US-09-336-447A-15
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US-08-913-942-4
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00541
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCLELand, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERNEX/POCKET NUMBER: 950811
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 10, Application US/08525742; Patent No. 5871742; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito, Shuji
Ohkawa, Setsuko
Saeki, Sakiko
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US-08-525-742-10
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Patent No.
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-421-868-2
US-09-541-782-6
US-09-268-347-30
US-09-268-347-30
US-09-268-347-48
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Maximum Match 100%
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PatentIn Release #1.0, Version #1.30
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; Pred. No. 3.4e-128;
10; Mismatches 7;
                                                                                                                                                                                                          APPLICATION NUMBER: PCT/JP94/00541
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCLEJAND, Le Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 950811
TELECOMMUNICATION INFORMATION:
TELEDRIONE: 202-659-2930
                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00541
                             UMBER: US/08/525,742
25-SEP-1995
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Patent No. 5871742;
GENERAL INFORMATION:
APPLICANT: Saito, Shuji
APPLICANT: Saeki, Sakiko
APPLICANT: Ohawa, Setsuko
APPLICANT: Ohawa, Ikuroh
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95.5%;
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Saeki, Sakiko
Ohsawa, Ikuroh
Funato, Hirono
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 610 amino acids TYPE: amino acid
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Matches 365; Conservative
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                                  APPLICATION NUMBER: FILING DATE: 25-SEP
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APPLICANT: Characa Statico
APPLICANT: Characa Statico
APPLICANT: Characa Statico
APPLICANT: Fundato Hirono
APPLICANT: Fundato Hirono
APPLICANT: Tatahashi, Kiyoohita
APPLICANT: Tatahashi, Kiyoohita
APPLICANT: Tatahashi, Kiyoohita
TITLE OF INVENTION: DOLYPEPTIDE, DNA ENCODING THE
TITLE OF INVENTION: RECOMBINANT VECTOR BEARING THE DNA AND
TITLE OF INVENTION: AS USE THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                           Score 1910; DB 2;
Pred. No. 3.8e-132;
3; Mismatches 4;
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Patent No. 5871742
GENERAL INFORMATION:
APPLICANT: Saito, Shuji
APPLICANT: Ohkawa, Setsuko
APPLICANT: Saeki, Sakiko
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IBM PC compatible
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Best Local Similarity 98.2%;
Matches 376; Conservative
                                                      LENGTH: 615 amino acids TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                     INFORMATION FOR SEQ ID NO:
                                        SEQUENCE CHARACTERISTICS
                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-742-10
     202-8870357
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STREET: 17
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301 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 337
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                                                                                                         RESULT 4
US-08-185-851A-4
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Best Local S
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          APPLICANT: Takahashi, "Bisohito TITLE OF INVENTION: NEW POLTPEPTIDE, DNA ENCODING THE TITLE OF INVENTION: NEW POLTPEPTIDE, DNA ENCODING THE TITLE OF INVENTION: RECOMBINANT VECTOR BEARING THE DNA AND TITLE OF INVENTION: RECOMBINANT VINUS UTILIZING THE RECOMBINANT VECTOR AS WELL NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
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                                                                                                                                                    ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND & ADDRESSEE: NAUGHTON
                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1638; DB 2;
Pred. No. 1.5e-112;
6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: PCT/JP94/00541
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     E: NAUGHTON
1725 K Street, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 95C
TELECOMMUNICATION:
TELEPHONE: 202-659-2930
Iritani, Yoshikazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.0%;
Best Local Similarity 95.5%;
Matches 322; Conservative 6
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SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
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amino acid
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COMPUTER READABLE FORM:
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CITY: Wa
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                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Saito, Shiji
APPLICANT: Ohkawa, Setsuko
APPLICANT: Initani, Yoshikazu
APPLICANT: Iritani, Yoshikazu
APPLICANT: Aoyama, Shigami
TITLE OF INVENTION: Poultry Mycoplasma Antigens, Gene
TITLE OF INVENTION: Thereof and Recombinant Vectors Cont
TITLE OF INVENTION: Well As Vaccines Utilizing the Same
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton STREET: 1725 K Street, N.W., Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS version 5.0
SOFTWARE: ASCII from Word Perfect version 5.1
APPLICATION DATA:
APPLICATION NUMBER: US/08/185,851A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.7%; Score 1612; DB 1;
95.0%; Pred. No. 1.2e-110;
iive 6; Mismatches 11;
327 YKLNNGNVQQVEFATSTSANNTTANPTQQLMRLKLLK 363
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R: PO-8-A930918
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NAME: Theresa M. Stevens-Smith
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: P0-8-A93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-659-2930
TELEPHONE: 202-687-0357
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                     Sequence 4, Application US/08185851A
Patent No. 5489430
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61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
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                                                              -----PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYG-PSTGYLYFPYKLVKAAD 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08293728D
Patent No. 6008341
GENERAL INFORMATION:
APPLICANT: FOSter, Timothy J.
APPLICANT: MODevitt, Damien L.
TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene FILE REFERENCE: 05344.105011
CURRENT APPLICATION NUMBER: US/08/293,728D
WUMBER OF SEQ ID NOS: 2.0
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22.8%; Pred. No. 0.001;
Live 57; Mismatches 154; Indels 114;
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Matches 96; Conservative
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LENGTH: 933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: tritani, Yoshikazu
APPLICANT: Tritani, Yoshikazu
APPLICANT: Takanashi, Yoshikazu
APPLICANT: Takanashi, Kiyoohita
APPLICANT: Takanashi, Kiyoohita
TITLE OF INVENTION: FOLYPEPTIDE, DNA ENCODING THE
TITLE OF INVENTION: POLYPEPTIDE, DNA ENCODING THE
TITLE OF INVENTION: RECOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
Gaps
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ZIP: 20006
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
FILING DATE: 25-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.3%; Score 806; DB 2; L
42.8%; Pred. No. 2.8e-51;
Live 62; Mismatches 123;
                                                                                                                                                                    327 YKLNNGNVQQVEFATSTSANNTTANPTQQLMRLKLLK 363
                                                                                                                            301 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 337
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FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00541
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: NAUGHTON
1725 K Street, Suite 1000
                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08525742
Patent No. 5871742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MCLELand, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 95(
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Saito, Shuji
APPLICANT: Oheava, Sectsuko
APPLICANT: Saeki, Sakiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Saeki, Sakiko
APPLICANT: Obsawa, Ikuroh
APPLICANT: Funato, Hirono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 661 amino acids
amino acid
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Best Local Similarity 42.8
Matches 185; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
STATE: DC
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58 TVNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL------VEAYKALK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 AHSKLKQVVEDFRKKFKTSEQVTPKKRLKRDLAANENNQQKI-----ELTVSPENI---- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 NYGPSTG---YLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANP-TPA 329
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                                                                                                                                                                                                             APPLICANT: Tai, Joseph Y.
APPLICANT: Tai, Joseph Y.
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group F TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDERSS: ADDRESSS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 ESLEQVEKELKHNSEA-----NLEDLVAKSKEIVREYEGKLNQSKNLP--ELKQLEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 INNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSADVIPVNYKYARRIVWNGDEPSSRILANINSIIDVSWIYSLAGINTKYQFSFS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8%; Score 136; DB 4; Length 103
22.7%; Pred. No. 0.063;
Live 51; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/923,992A FILING DATE: 05-SEP-1997 CLASSIFICATION: 536
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 Sequence 8, Application US/08923992A Patent No. 6280738 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2610
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1098 amino acids
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Best Local Similarity 22.7%
Matches 84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                    363 KTVLVDYEKYGKFYNLSIKGTIDQIDKTNNTYRQTIYVNPSGDNVIAPVLTGNLKPNTDS 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 NNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SITQDISTEATPSNNESAPQSIDASNKDVVNQAVNTSAPRMRAFSLAAVAADAPAAGTDI 232
207 ANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAG-TN 265
                                               ---IMAGDQ----VLANGVIDSDGNVIYTFTDYVN 324
                                                                                                        266 TKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTAN 325
                                                                                                                                               326 PTPAVDEIKVAKI-----VLSGLRFGQNTIELSVPTGEGNMNKVAPMI-GNIYLSSNE 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ASSLITKTLDPLNGGTLL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 DSNEITTANKNINNTLSTINEQ----KTN-ADALSNSFIK----KVIQNNEQSFVGTFTN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 ANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAG-TN 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 AKVPP------IMAGDQ-----VLANGVIDSDGNVIYTFIDYVN 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 TKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTAN 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325 TKDDVKATLTMPA--YI------DPENV-----KKTGNV-----TLATGIGSTTAN 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09421868
; Batent No. 6177084
; GENERAL INFORMATION:
    APPLICANT: Foster, Timothy J.
    APPLICANT: McDevitt, Damien L.
    TITLE OF INVENTION: a uzeus Fibrinogen Binding Protein Gene
    FILE REFERENCE: 05344.105011
    CURRENT APPLICATION NUMBER: US/09/421,868
    CURRENT FILING DATE: 1999-10-19
    PRIOR APPLICATION NUMBER: 08/293,728
    PRIOR APPLICATION NUMBER: 08/293,728
    NUMBER OF SEQ ID NOS: 20
    NUMBER OF SEQ ID NOS: 20
    SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.0%; Score 159; DB 4; Length 933;
Best Local Similarity 22.8%; Pred. No. 0.001;
Matches 96; Conservative 57; Mismatches 154; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 MSITKKDANPNNGQTQL--EAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETV 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Staphylococcus aureus US-09-421-868-2
                                                     292 AKVPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JJS-09-421-868-2
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CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 24
LENGTH: 1002
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                                                                                                                                                  ; ORGANISM: Haemophilus influenzae US-09-268-347-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
FILE REFERENCE: 1038-860
                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 91; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
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                                                                                                                                  TYPE: PRT
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APPLICANT: LOOSMOre, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
611 NGYFTLLNDFNASMEELLNTHSNQLLISMTKITEHFQSLDEALQSARSSCAVPNSSLDLI 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 LEQLKMAKTNLESAINQANTDKTTFDNEHPN----LVEAYKALKTT---LEQRATNLEG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     731 LOHTHEESOKELMYGVRNDIDALVKTCTTSLNDADIILSDYISDOKSKFESKQQDLIANI 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 NKNINNTLSTINEQ-KTNADAL----SNSFIKK---VIQNNEQSFVGTFTNANVQPSN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 QVE----FATSTSANNTT------ 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 NGQ-TQLEAARMELTDLINAKA-MTLASL----QDYAKIEASLSSAYSEAETVNNNLNAT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 YSFVAFSADVTPVNYKYARRTVWNG----DEPSSRILANTNSITDVSWIYSLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----FSFSNYGPSTGYLYFPYKLVKAADANNVGL--QYKLNNGNVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.8%; Score 135.5; DB 4; 20.9%; Pred. No. 0.066; tive 76; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                            APPLICANT: Sakowicz, Roman
PPLICANT: Berand, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEO ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/09268347 Patent No. 6335182
                                                                                                                                                                                    Sequence 6, Application US/09541782
Patent No. 6284480
GENERAL INFORMATION:
APPLICANT: Nislow, Corey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 20.9% ses 97; Conservative
                                                      330 VDEIKVAKIV 339
                                                                                          510 OKDSKTEEKV 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: S.pombe
US-09-541-782-6
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SEQ ID NO 6
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479 LVDSLNKLGWKVGVGKDGTGATDGTHTDTLVKSGDKVTLKAGDNLKVKQEGTNFTYVLRD 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 KYARRIVWNGDEPS-----SRILANTNSITDVSWIYS---LAGINTKYQFSFSNYG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        630 DNAYKGLTNLDEKSKGKQTPTVADNTAATVGDLRGLGWVISADKTTGESKEYSAQVRNAN 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TILLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group B TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
                                                                        Gaps
                                                                                                                                         13 NGQTQLEAARM----ELTDLINAKAMTLASLQDYAKIEASLSSAYSE-----AET 58
                                                                                                                                                                                                                                                                              59 VNNNLNATLEQLKMAKTNLESA------INQANTDKTTFDN-----EHPN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | : | : | : | : | 133 -----AIAFGSGSKALRDNIVAIGTGNVVNAEKSGAFGDPNYIEDKAGGSYAFGNDN 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 KIVLSGLRFGQNTIEL---SVPTGEGNM------NKVAPMIGNIYLSSNEN 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SGLKKFGDANFNP----LTSSADNLTKQY
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   Length 1002;
                                                                        Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
ch 6.6%; Score 132.5; DB 4;
1 Similarity 19.1%; Pred. No. 0.1;
91; Conservative 58; Mismatches 153;
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6.6%; Score 131; DB 4; Length 1004; 20.2%; Pred. No. 0.13;
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APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY_AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08923992A Patent No. 6280738 GENERAL INFORMATION:
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                                      97; Conservative
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MEDIUM TYPE: Floppy
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Query Match
Best Local Similarity
Matches 97; Conserv
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TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 SLEQVEKELKHNSEA-----NLEDLVAKSKEIVREYEGKLNQSKNLP--ELKQLEEER 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 KKDANPNNGQTQLEA-ARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AET 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 SADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFS----N
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                                                                                                                                                                                                                                                                                                                                                                                           Length 1164;
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                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                51; Mismatches 157;
                                                                                                      REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELEPHONE: (202) 371.2600
TELEPHONE: (202) 371.2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                             6.6%; Score 131.5; D 22.8%; Pred. No. 0.15;
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CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VET. 2.0
               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :09-268-347-30
Sequence 30, Application US/09268347
Patent No. 6335182
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US-09-268-347-30
 05-SEP-1997
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Matches 84; Conservative
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MOLECULE TYPE: protein

US-08-923-992A-2
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548 KDSKTEEKV 556
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LENGTH: 1004
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22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 INNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV 226
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APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group B TITLE OF INVENTION: Streptococcal Beta Antigens
CORRESPONDENCES: 34
CORRESPONDENCE ADDRESS:
      Gaps
                                                                                                                                                                                                                                                                                                                                  94 -EHPNLVEAYKAL------EQRATN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 NYKYARRTVWNGDEPS----SRILANTNSITDVSWIYSLAGT----NTKYQFSFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | : | : | : | : | 531 YALKDELTDVKSVEFKDTANGA--------
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51; Mismatches 152; Indels 180;
                                                                 13 NGQTQLEAARM----ELTDLINAKAMTLASLQDYAKIEASLSSAYSEA--
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                                                                                                                                                                                                59 VNNNLNATLEQLKMAKTNLESAINQANTDKTTF------DN----
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
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REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
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TVNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLE 117
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATEULL VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TDNHKIAE 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 IVLSGLRFGQN-TIELSVPTGEGNM------NKVAPMIGNIYLSSNENNADKI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : |: |: |: | : | : | 469 IIIKNLKLNQSQIVTLKAKDDSGNVVEKTFTIIVQKKEEKQVPKTPEQKHSKTEQNVPQE 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 VNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL------VEAYKALKT 107
                                                                                                                                                                                                                                                                                                                                                                               108 TLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNI 167
                                                                                                                                                                                                                                                                                                                                                                                                                314 SLEQVEKELKHNSEA-----NLQDLVAKSKEIVREYEGKLNQSKNLP--ELKQLEEEA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------TVYEGEDVKFTVTAKSDS------KTTLDFSDLLTKYNP 447
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                    6 KKDANPNNGQTQLEA-ARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AET 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ITKKDAN-----PNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNTLSTINEQ-----KTNADALSNSFIKKVI---ONNEQSFVGTFTNANVQPSNYSFVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 HSKLKQVVEHFRKKFKTSEQVTPKKRVKRDLAANENNQQKI-----ELTVSPENI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SADVIPVNYKYARRTVWNGDEPSSRILLANTNSITDVSWIYSLAGTNTKYQFS--FSNYGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92;
                                                                                                                                                             6.6%; Score 131; DB 4; Length 1104;
20.2%; Pred. No. 0.15;
tive 50; Mismatches 154; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 2048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 6.5%; Score 129; DB 4; Length 20. Best Local Similarity 21.2%; Pred. No. 0.48; Matches 83; Conservative 60; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SV-----SDRISTNYKTN-----
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Patent No. 6335182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Haemophilus influenzae
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
                                                                                                                                                                                Best Local Similarity 20.2
Matches 85; Conservative
                                                                     TOPOLOGY: 11near
MOLECULE TYPE: protein
US-08-923-992A-4
                                                        TYPE: amino acid
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LENGTH: 2048
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                                                                                                             GLSSTAYNQIRNNLVDLYNKA--SSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTIN 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 WNGDEPSSRILANTNSI--TDVSWIYSLAGTN--TKYQFSFSNYGPSTGYLYFPYKLVKA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 ADANNYGLQYKLNNGNYQQVEFATSTSANNTTANPTPAVDEIKVAKIVL-SGLRFGQNTI 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08923992A
Patent No. 6280738
GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group B TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                           344 AVN------VAQLEAVVKWAKERRITFQGD-DNSTDVKIGLDNTL----TIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 SSSTTABLLSDSL-----TFTQPN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             457 -TGSQSTSKTVYGVNGVKFTNNAETTAAIGTTRITRDKIGFARDG-DVDEKQAPYLDKKQ
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1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/923,992A FILING DATE: 05-SEP-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.3%; Score 126.5; DB 4; Best Local Similarity 22.5%; Pred. No. 0.32; Matches 83; Conservative 51; Mismatches 158;
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDABR: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.014000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1128 amino acids
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59 VNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL------VEAYKALKT 107
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254 LONLAQKSLEELDKATIN-----EQATQVKNQFLENAQKLKEMQPLIKETNVKLYKAMSE 308
                                                                                                            108 TLEORATNLECLSSTAYNQIRNNLVDLYNKASSLITÄTLDPLNGGTLLDSNEITTANKNI 167 :: : | | | | | : : :
                                                                                                                                :||| |: | | || |: : : || || |: :: 359 SLEQVEKELKHNSEA-----NLEDLVAKSKEIVREYEGKLNQSKNLP--ELKQLEEEA 359
                                                                                                                                                                      168 NNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVAF 219
                                                                                                                                                                                       220 SADVIPVNYKYARRIVWNGDEPSSRILANINSIIDVSWIYSLAGINIKYOFSFS----N 274
                                                                                                                                                                                                                                              410 ------TVYEGEDVKFTVTAKSDSKTTLDFSDLL----TKYNPSVSDRISTN 451
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June 12, 2002, 10:47:42; Search time 17.44 Seconds (without alignments) 872.522 Million cell updates/sec
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1998
1 CMSITKKDANPNNGQTQLEA......SSNENNADKIPGYRRPGTFL 393
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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105224 Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

.Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	pti		_	saccharom			P47580 mycoplasma		-		Q00174 drosophila		P32618 saccharomyc	Q12355 saccharomyc			P54674 dictyosteli	-	P34278 caenorhabdi	P14738 staphylococ	P40957 saccharomyc	P34231 saccharomyc			Q09904 schizosacch		P04931 plasmodium	lactococ	P46590 candida alb	P80544 staphylococ			P53753 saccharomyc	
SUMMARIES	ID	NISP_LACLA	AR56_CANAL	SW11_YEAST	YM41_YEAST	CUT7_SCHPO	Y338_MYCGE	BAG_STRAG	RBP2_PLAVB	WAPA_BACSU	LMA_DROME	YIQ9_YEAST	YEF3_YEAST	PST1_YEAST	MSP1_PLAFK	MSP1_PLAFW	P3K2_DICDI	LIN5_CAEEL	YKK1_CAEEL	FNBA_STAAU	MAD1_YEAST	YKS7_YEAST	NSP1_YEAST	MYSP_SCHJA	N124_SCHPO	CAT8_YEAST	ARP_PLAFA	P2P_LACLC	ALS1_CANAL	MRSP_STAAU	USO1_YEAST	FLIC_SALON	YN96_YEAST	PMPB_CHLMU
	DB	٦	Н	П	Н	П	-	Н	П	Н	-	Н	Н	П	Н	-	-	П	П	Н	Н				-	-	-	-	-	~	-	-		
	Query Match Length	682	857	1314	719	1085	1271	1164	1251	2334	3712	995	926	444	1630	1639	1858	821	1010	1018	749	750	823	866	1159	1433	537	1902	1260	1637	1790	507	1117	1672
d	Query Match				6.9				6.5	6.4	4.9	6.4																				6.1		6.1
	Score	154.5	143	138.5	137	135.5	132	131.5	129	128.5	128.5	128	127	126.5	126.5	126.5	125.5	124.5	124.5	124.5	124	124	124	124	124	124	123.5	123.5	123	123	123	122.5	122	122
	Result No.	-	7	3	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

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88888888

P38272 saccharomyc	054001 salmonella 009625 caenorhabdi	P49022 lactococcus P41508 mycoplasma	P28742 saccharomyc Q02470 lactobacill	Q02945 equine rota P25146 listeria mo	P11657 streptococc P19880 saccharomyc
YBYO_YEAST	TOLC_SALEN	PIP_LACLA	KIP1_YEAST P2P_LACPA	VP4_ROTEH INLA_LISMO	PAC_STRMU PDR4_YEAST
٦.					п п
425	491	901	1111	776 800	1565 650
6.1	9.0	9 9	6.1	0.0 0.0	6.0
121.5	121	121	121	120.5	120.5
34	36	8 6	40	42	44

## ALIGNMENTS

RESULT NISP L	RESULT 1
A P	NISP_LACLA STANDARD; PRT; 682 AA.
불분	01-FEB-1995 (Rel. 31, Created)
: 동 등	(Rel. 40, Last annotation update)
H H	Nisin leader peptide processing serine protease NiSP precursor (EC 3.4.21).
N 6	NISP.
၈ ဗ	Lactococcus lactis (subsp. lactis) (streptococcus lactis). Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
8	
N C	NCB1_T8X1D=130U; [1]
RP	SEQUENCE FROM N.A.
Z Z	STRAIN=NIZO R5; MEDLINE=93239683: PubMed=8478324;
RA B	van der Meer J.R., Polman J., Beerthuyzen M.M., Siezen R.J.,
КA	Kuipers O.P., de Vos W.M.;
F.	"Characterization of the Lactococcus lactis nisin A operon genes
Z &	nisk, encoding a subrilisin-like serine protease involved in precursor processing, and nisk, encoding a regulatory protein
R	6
Z.	J. Bacteriol, 175:2578-2588(1993).
N C	[2]
אַ עַ הַ	SECULENCE FOR N.A.
Z X	
ΚA	Engelke G., Gutowski-Eckel Z., Kiesau P., Siegers K.,
R'A	Hammelmann M., Entian KD.; "Requisity in Lactococcus lactis"
RT	
RI.	Appl. Environ. Microbiol. 60:814-825(1994).
RP	3D-STRUCTURE MODELING.
RX	MEDLINE=95357326; PubMed=7630881;
A P	Siezen R.J., Rollema H.S., Kuipers O.P., de Vos W.M.; "Homology modelling of the Lactococcus lactic leader neptidase Nisb
R.	
RL	ein Eng. 8:117-125(1995).
ဗ္ဗ	FUNCTION: CLEAVES THE
3 8	-!- FATHWAY: LAST STEP OF NISIN BIOSINIHESIS. -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL
ខ	
ខ្លួ	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
ខ្ល	-!- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
ပ္ပ	IN THE REGION OF THE MEMBRANE ANCHOR.

Candida albicans (Yeast).

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13;
                                                                                                                                                         MENUNCIS SOG. 20. 20. 4. 1 PRRO10199; Gram_pos_anchor. InterPro; IPR001209; Peptidase_S8. 1.  
InterPro; IPR001209; Peptidase_S8. 1.  
PRINTS; PR00723; SUBTILISIN.  
PROSITE; PS00136; SUBTILIASE_ASP; 1.  
PROSITE; PS00138; SUBTILIASE_HIS; 1.  
PROSITE; PS00138; SUBTILIASE_RIS; PALSE_NEG.  
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.  
Hydrolase; Serine protease; Cell wall; Signal; Transmembrane; Zymogen.  
SIGNAL  
22  
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELULAR (POTENTIAL).

EXTRACELULAR ARCHOR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 LRQPLKNQKVEAQPLLISNSSEKKASVYTNSHDFWDYQW------DMKY---VTNNGES 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 ETVNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 EGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINE 176
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NNOV-1997 (Rel. 41, Last annotation update)
ARG5.6 protein, mitochondarial precursor [Contains: N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase); Acetylglutamate kinase (EC 2.7.2.8) (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NISIN LEADER PEPTIDE PROCESSING SERINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91;
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D5F29313F2983EC9 CRC64;
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email to license@isb-sib.ch).
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                                                       EMBL; L11061; AAA25200.1; -. EMBL; X76884; CAA54210.1; -.
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Best Local Similarity 21.0
Matches 75; Conservative
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                                                                                                              HSSP; P29600; 1GC
MEROPS; S08.059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
                                                                                                                                                                                                            Microbiology 143:297-302(1997).

-!- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+) + phosphate = N-acetyl-5-glutamyl phosphate + NADPH.

-!- CATALYTIC ACTIVITY: ATP + N-acetyl-L-glutamate = ADP + N-acetyl-L-glutamate 5-phosphate.

-!- CATALYTIC ACTIVITY: ATP + N-acetyl-L-glutamate = ADP + N-acetyl-L-glutamate 5-phosphate.

-!- SEMECLEGLAR LOCATION: ALCOCHODIAL.

-!- SEMECLAGLAR LOCATION: Microchodrial.

-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE ACETYLGLUTAMATE KINASE FAMILY.

-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE NAGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 ASSLITKTLDPLNGGTLLDSNEITTANKNIN-NTLSTINEQKTNADALSNSFIKKVIQNN 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 K----TTFDNEHPNLV-EAYKALKTTLEQR-----ATNLEGLSSTAYNQIRNNLVDLYNK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 IEASLSSAY----SEAETVNN---NLNATL------EQLKMAKTNLESAINQANTD 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 VEAAINSGYLPILTSLAETSSGQLLNVNADVAAGELAREFEPLKIVYLNEKGGIINGNTG
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                                                                                                SEQUENCE FROM N.A.
STRAIN-BATCC 64385 / 1001;
MEDLINE-97195775; PubMed=9043106;
Negredo A., Monteoliva L., Gil C., Pla J., Nombela C.;
Negredo A., Monteoliva and one-step disruption of the ARG5,6 gene of Candida albicans.";
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58; Mismatches 134; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodom; PD003765, AGPR_act_site; 1.
PROSITE; PS01224; ARGC; 1.
Oxidoreductase; Transferase; Kinase; Arginine biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.2%; Score 143; DB 1; Length 857; 23.3%; Pred. No. 0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion; Multifunctional enzyme; Transit peptide.
TRANSIT 1 7 MITOCHONDRION (POTENTIAL).
CHAIN ? ? ACETYLGLUTAMATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE2CEAD8FF8C4C71 CRC64;
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InterPro; IPR001048; Aakinase.
InterPro; IPR000534; Semialdh_dh.
Pfam; PF00656; aakinase; 1.
Pfam; PF01118; Semialdhyde_dh; 1.
Pfam; PF02774; Semialdhyde_dhc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DEHYDROGENASE FAMILY.
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Best Local Similarity 23.3
Matches 99; Conservative
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857 AA;
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                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Transcription regulatory protein SWII (SWI/SNF complex component SWII)
(Transcription regulatory protein ADR6) (Regulatory protein GAM3).
ADR6 OR SWII OR GAM3 OR YPL016W OR LPAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ø
 ---KLVKAADANNVG--LQYKLNNG---NVQQVE-FATSTSANNTTANPTP 328
                                                                  AVDEIKVA---KIVLSGLR--FGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 383
                                                                                        FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION. THE SWI/SNF COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER OF GENES. THIS COMPLEX ALTERS CHOMATIN STRUCTURE TO FACILITATE BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACTORS. SUBUNIT: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-89057455; PubMed-3143101; O'Hara P.J., Horowitz H., Elchinger H., Young E.T.; "The yeast ADRG gene encodes homopolymeric amino acid sequences and potential metal-binding domain."; Nucleic Acids Res. 16:10153-10170(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation; Activator; DNA-binding; Nuclear protein;
21nc-finger.
                  Peterson C.L., Herskowitz I.; "Characterization of the yeast SWI1, SWI2, and SWI3 genes, which encode a global activator of transcription."; Cell 68:573-583(1992).
                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 65 ASN/THR-RICH.
1347 1258 GLN-RICH.
121 1258 C4-N'FRICH.
1314 AA; 147938 MW; F442D5A82013CDBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                 PRT; 1314 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92154671; PubMed-1339306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U33335, AAB68089.1; -.
EMBL, X12493; CAA31013.1; -.
PIR, S05728; TNBYR6.
TRANSFAC, T01279; -.
SGD, S0005937; SW11.
Interpro; IPR001606; ARID.
PF031388; ARID; 1.
SMART; SM00501; BRIGHT; 1.
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-4932;
                                                                                                                                         384 PGYRR 388
                                                                                                                                                                            QGYNK 579
283 YFPY---
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P09547;
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SEQUENCE
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                                                                                                      57 NTNNNNTNTGASGVD------DFQNFFDPRPFDQNLDSNNNNSNSNNNNS--N 104
                                                                                                                                                                                                                                                       DEPSSRILLANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVG 298
                                                                                                                                                                                                                                                                                                                                                                                                                            248 NLTSNQLISN-----SDNNNNS 285
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                                                                          10 NPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNATLEQ
                                                                                                                                                    70 LKMAKTNLES---AINQANTDKTT-----FDNEHPNLVEAYKALKTTLEQRATNLEGL
                                                                                                                                                                                           105 TVASSTNFTSPTAVVNNAAPANVTGGKAANFIQNQSPQFNSPYDSNNSN----TNLNSL
                                                                                                                                                                                                                                 SSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKT
                                                                                                                                                                                                                                                                                                                               2 MSITKKDANPNNGQTQLEAARMELTDL------INAKAMTLAS-----
                                                                                                                                                                                                                                                                                                           180 NADALSNSFIKKVIQNNEQSFVGTFTNANVQP-SNYSFVAFSADVTPVNYKYARRTVWNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.9%; Score 137; DB 1; Length 719;
19.8%; Pred. No. 1.1;
tive 72; Mismatches 175; Indels 178;
  Length 1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 79.4 kDa protein in ALDZ-DDR48 intergenic region.
YMR172W OR YM8010.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
STAIN=S288C / A. Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4652BE93743D5A54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 NNHNMRNNSNNKTSNNNNVTAVPAATPANTNNSTSNANTVFSE 328
  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 LOYKL-----NNGNVQQVEFATSTSANNTTANPTPAVDE
6.9%; Score 138.5; D
20.4%; Pred. No. 1.9;
iive 56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     719 AA
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                                      Conservative
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Hypothetical protein.
SEQUENCE 719 AA; 7941
                Best Local Similarity
Matches 70; Conserv
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  Query Match
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YM41_YEAST
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                                                              97 LLRTSAAISAPTGTSQPTETIGEKLSNEERVNSNVSASNSTTAGTGRMLSQSLTN-DSPS 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hagan I., Yanagida M.;
"Novel potential mitotic motor protein encoded by the fission yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 NDHASAAQKPISALSPLINSHNSTISMNYINSSIHSGVISASNSFHDLNSLNNFGTITAL
                                                                                                                                                                         216 KLVAQPSARPSTNNAQNKLAIELLNSISAVSSAYLQKMQNNGSGRQHTADLCTGDSNTHS
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-LQDYAKIEA-----SLSSAYSEAETVNNNLNA------TLEQLKMAKTNLESAI
                                                                                                                                                                                                                                                                   ----NGTLDSNEITTANKN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 GLRFGONTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKIPGYRRPGT 391
                                                                                                                                NQANTDK - - - - TTFDNEHPNLV - - - EAYKALKTTLEQRATNLEGLSSTAY -
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1992 (Rel. 21, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                -----INNTLSTINEQKTNA-----
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01-OCT-1996
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                                                                                                                                                                                                                                           PRINTS; PRUDJOSO, DOMAIN; 1.

PROSITE; PS0041; KISC; 1.

PROSITE; PS0067; KINESIN_MOTOR_DOMAIN; 1.

PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.

MOTOR protein; Cell division; Microtubules; ATP-binding; Coiled coll; Mitosis; Cell Givision; Repeat.

DOMAIN 716 436 604 COILED COIL (POTENTIAL).

DOMAIN 715 740 COILED COIL (POTENTIAL).

PROSITE PROSITE COILED COIL (POTENTIAL).

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VSELKDSKNSLLDALEHSLQDISMSSQKLGNGISSELIELQKDMKESYRQLVQELRSLXN 742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 QVE----FATSTSANNTT------350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 LEQLKMAKTNLESAINQANTDKTTFDNEHPN----LVEAYKALKTT---LEQRATNLEG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKNINNTLSTINEQ-KTNADAL----SNSFIKK---VIQNNEQSFVGTFTNANVQPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 YSEVAFSADVIPVNYKYARRIVWNG----DEPSSRILANINSIIDDVSWIYSLA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         954 ----ASQAEIVGANKERIQKTVENGSQLLDSKSKAIHSNSRSMYD----HCLALAESQKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8%; Score 135.5; DB 1; Length 1085; 20.9%; Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY CDC2) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
SASNPRKRREPPTIDTGYPDRSDTNSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEIT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1023 WTRDSSLIKETTNLNLDSDKKFVRETYTSSNQTNEPDV--YDKP 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 2.2; 76; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein MG338 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā
                                                                            EMBL; 270691; CAA94636.1; -... PIR; S14032; S14032.1 interpro; PR001752; kinesin. Pfam; PF00225; kinesin. PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 33, Created)
(Rel. 33, Last sequ
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1085 AA; 122133
                                                         EMBL; X57513; CAA40738.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 20.9 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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01-FEB-1996
16-OCT-2001
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P47580;
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Y338_MYCGE
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SIT--DVSWIYSLAGTUTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNV 308
                                                                                                                                                                                                                                                            Streptococcus.
NCBI_TaxID=1311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1164
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01-AUG-1992
                                                                                                                                          BAG_STRAG
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PETAIN-ATCC 33530 / G-37;

MEDLINE-96026346; PubMed-756993;

MEDLINE-96026346; PubMed-756993;

Praser C.M., Gocayne J.D., White C., Adams M.D., Clayton R.A.,

Flaischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene conjement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANK--NINNTLSTIN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 GTSSNL-----NPLDKFIKSSSATTVMMK----SAMTKSQEVTSDNNGFNVKSEFLKIN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 PSLSSSGSDNSSNTQSFWKQVQALNNSSQTATIFDAVRMESNSSQAQVVTSNLLVSLSSK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLE-----QLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E--QKTNADALSN--SFIKKVIQNNEQSFVGTFTNANVQPSNYS------FVAFSAD 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 VTPVNYKYARRTVW-NGDE-----ILANTN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TT---QKQQQKPVYVRGDDAIYAFHIDGGNYFLENSSPNKRNFEKQAEVLLMRFLQGQTN 532
                                                                                                                                                                                                                                                                                                  sequencing.";
J. Bacteriol. 175:7918-7930(1993).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 KDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAK-IEASLSSAYSEAETVNNNLNA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98;
                                                                                                                                                                                                                                            STRAIN-ATCC 33530 / G-37;
MEDLINE-9407520; Pubmed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                        Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                        (Potential).
SIMILARITY: BELONGS TO THE MG307 / MG309 / MG338 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL LIPOPROTEIN MG338.
N-ACYL DIGLYCERIDE (POTENTIAL).
W; FCE6042067310A70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.6%; Score 132; DB 1; Length 1271; 22.2%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 4.1;
57; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Lipoprotein; Membrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142492 MW;
                                                                                                                                                                                                                                 SEQUENCE OF 1023-1114 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U39715; AAC71563.1; -.
                                      Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                       Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U01809; AAD12341.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26
1271
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             qenitalium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 84; Conserv
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                                               NCBI_TaxID=2097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; MG338
            Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIPID
SEQUENCE
                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE DOMAIN.
IGA-BINDING (POTENTIAL).
IGA-BINDING (POTENTIAL).
PRO-RICH REPEATS.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
two
                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jerlstroem P.G., Chhatwal G.S., Timmis K.N.;
"The IgA-binding beta antigen of the c protein complex of Group B streptococci: sequence determination of its gene and detection of binding regions.";
Mol. Microbiol. 5:843-849(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGA FC RECEPTOR.

EXTRACELLULAR (POTENTIAL).

MEMBRANE ANCHOR (POTENTIAL)

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEINS.
W: 65DE94AF720A5474 CRC64;
                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19A FC receptor precursor (Beta antigen) (B antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Repeat; Signal;
                                                                                                                                                                                                                                  1164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 38-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00343; GRAM POS_ANCHORING; 1.
Cell wall; Transmembrane; Receptor; Repedimentoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S15330; FCSOAG.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003599; I9.
                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00746; Gram_pos_anchor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=LA239;
MEDLINE=91312121; PubMed=1857207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION OF IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA; 131051 MW;
                                                              309 QOVEFATSTSANNTTANPT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X59771; CAA42442.1; -.
                                                                                                            584 DVCDLAKKLLKNNTNLSET
                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus agalactiae.
                                                                                                                                                                                                                                  STANDARD;
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1131
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438
826
945
1137
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Gaps

Indels 122;

Mismatches 140;

70;

Conservative

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                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO HUMAN RETICULOCYTE CELLS.
-1- SUBCELLULAR LOCATION: Membrane-bound (Probable).
                                                                                                                                                                                                                                              445
                                                                                                                                                                                                                                                                                                    487
                                                                                                                                                                                                                                                                                                                              YGPSTG---YLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANP-TPAV 330
                                                                                                                                                                                                                                                                                                                                              TLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNI 167
                                                                      ----VEAYKALKT 107
                                                   6 KKDANPNNGQTQLEA-ARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AET 58
                            Gaps
                                                                                                                                                                                 SLEQVEKELKHNSEA------NLEDLVAKSKEIVREYEGKLNQSKNLP--ELKQLEEEA
                                                                                                                                                                                                                   NNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVAF
                                                                                                                                                                                                                                   396 HSKLKQVVEDFRKKFKTSEQVTPKKRVKRDLAANENNQQKI-----ELTVSPENI----
                                                                                                                                                                                                                                                                         SADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGINTKYQFSFS-----N
                                                                                                                                                                                                                                                                                            Length 1164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium vivax (strain Belem).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=31273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barnwell J.W.;
Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54BA51C7404AC572 CRC64;
                            Indels
  DB 1;
6.6%; Score 131.5; DB 1;
22.8%; Pred. No. 3.9;
tive 51; Mismatches 157;
                                                                                                            59 VNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25, Last sequence update) 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galinski M.R., Medina C.C., Ingravallo P., "A reticulocyte-binding protein complex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Last annotation upda
Reticulocyte binding protein 2 (Fragment).
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1251 AA; 143741 MW;
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01-APR-1993 (Rel. 25, Last sequ
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                              84; Conservative
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Cell 69:1213-1226(1992)
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Q00799;
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Length 1251;

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573 INDYENKMGE-----IYNEFEGSLNKISEN-----LRNASENTSDYN----SAKT 613
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                           QTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAE-----TVNNNLNAT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=168 / BGSCIA1;
MEDLINE=95219088; PubMed=7704263;
Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
Tochida and sequencing of a 29 kb region of the Bacillus subtilis genome containing the hut and wapA loci.";
Microbiology 141:337-343(1995).
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MEDLINE-97124196; PubMed-8969509;
MEDLINE-97124196; PubMed-8969509;
Mixer Y., Fujita Y.;
Riyata Y.; Fujita Y.;
"Sequencing of a 65 kb region of the Bacillus subtilis genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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01-MAR-2002 (Rel. 41, Last annotat
Wall-associated protein precursor.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
containing the lic and cel loci, and creation of a 177 kb contig
covering the gnt-sacxY region.";
Microbiology 142:3113-3123(1996).
-!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
MOTILITY, SECRETION OR DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED
INTO THE MEDIUM.
                                                                                                                              SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
                                                                             -!- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE
                                                                                                                                                                                                                                                                                                                                                                                                                                     1-3.
31 x 21 AA APPROXIMATE TANDEM REPEATS OF
44)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
2-1.
                                                                                            101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED MOTIF REPEATED 31 TIMES.
                                                                                                                                                                                                                                                                                                                                                                                         3 X 101 AA APPROXIMATE TANDEM REPEATS 1-1.
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1 28 OR 32 (POTENTIAL).
29 2334 WALL-ASSOCIATED PROTEIN.
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EMBL; D31856; BAA0656.1; -.
EMBL; D29985; BAA06560.1; -.
EMBL; D83026; BAA11683.1; -.
EMBL; 299124; CAB15959.1; -.
PIR; S32920; S32920.
Subtilist; BG10797; wapA.
InterPro; IPR003305; CBD_6.
Pfam; PPC0218; CBD_6; 1.
Cell wall; Repeat; Signal; Comp
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MEDLINE-92078147; Pubmed-1744083;
Garrison K., Mackrell A.J., Fesslar J.H.;
Drosophila laminin A chain sequence, interspecies comparison, and
domain structure of a major carboxyl portion.";
J. Biol. Chem. 266:22899-22904(1991).
-!- FUNCTION: BINDING TO CELES VIA A HIGH AFFINITY RECEPTOR, LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
                                                                                        1829 FTYNKLDQMIEMKDSTSSYSFDYDENGNVQTFIT-GNGGGTSFSYDERNLVSSLHIGDKN 1887
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                                     Gaps
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                                                                   3 SITKKDANPNNGQTQLEAARM-ELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN- 60
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"Genetic analysis of laminin A reveals diverse functions during
norphogenesis in Drosophila.";
                                     113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fessler J.H.; "Laminin A chain: expression during Drosophila development and
   Length 2334;
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MEDLINE-93049203; PubMed-1425586;
Kusche-Gullberg M., Garrison K., Mackrell A.J., Fessler L.I.,
                                   Indels
   DB 1;
                                   152;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
Laminin alpha chain precursor.
LANA OR LAMA.
6.4%; Score 128.5; I 22.1%; Pred. No. 14; iive 56; Mismatches
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MEDLINE=94038678; PubMed=8223265;
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EMBO J. 11:4519-4527(1992).
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                                                                                                                           DOMAIN
                          CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
MITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
COMPLETE LOSS-OF-FUNCTION BURRIE MORSPHILA.
COMPLETE LOSS-OF-FUNCTION MUTATIONS LEAD TO LATE EMBRYONIC
LETHALITY. CERTAIN PARTIAL LOSS-OF-FUNCTION MUTATIONS GIVE RAISE
TO ESCAPER ADULTS, WHICH HAVE ROUGH BYES ASSOCIATED WITH CHANGES
IN CELL FATE AND PATTERN, MISSHAPPEN LEGS AND DEFECTS IN WING
STRUCTURE.
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, BETA, BETA, BULCH BE BOUND
TO EACH OTHER BY DISGLIFIDE CHAINS (ALPHA, BETA, BETA, BETA, BETA, BULCH BE BOUND
TO EACH OTHER BY DISGLIFIDE CHAINS (ALPHA, BETA, BETA, BETA, BETA, BULCH BE BOUND
TO EACH OTHER BY DISGLIFIDE CHAINS (ALPHA, BETA, BETA, BETA, BACH BUD.
COMPRESION ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH BUD.
TO SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
MEMBRARES (MAJOR COMPONENT).
TISSUE SPECIFICITY: NUMLY FORMED MESODERM AND LATER PROMINENTLY
COMPANIAL STAGE: DURING MORPHOGENESIS, MOSTLY IN EMBRYO
DEVELOPMENTAL STAGE: DURING MORPHOGENESIS, MOSTLY IN EMBRYO
DEVELOPMENT AT 10-12 HOURS.
COMPANIS THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
MITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
COMPANIS CONTAINS 11 LAMININ DOMAIN IV (DOMAIN VI).
CONTAINS 21.5 LAMININ DOMAIN IV (DOMAIN IV, IS NOT STRUCTURE STR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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EMBL; M96388; AAC37178.1; ...

EMBL; M75882; AAA28662.1; ...

EMBL; M75882; AAA28661.1; ...

EMBL; M75882; AAA28661.1; ...

ELYBASe; FURNO00226; LanA.

InterPro; IPR0000361; EGF-1ike.

InterPro; IPR001034; Laminin_B.

InterPro; IPR001034; Laminin_B.

InterPro; IPR001034; Laminin_B.

InterPro; IPR001034; Laminin_B; 1.

Efam; PF00052; laminin_B; 1.

Pfam; PF00053; laminin_B; 1.

Pfam; PF00053; laminin_Nterm; 1.

PRINTS; PR0011; EGFLAMININ.

PRODOM; PD003031; Laminin_B; 1.

PRODOM; EGF_Lam; 1.

SMART; SM00180; EGF_Like; 1.

SMART; SM00180; EGF_Like; 1.

SMART; SM00186; EGF_1; 1.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01025; LAMININ_TYPE_EGF; 19.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01186; EGF_1; 17.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01186; EGF_1; 17.

PROSITE; PS01186; EGF_1; 17.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01186; EGF_1; 17.

PROSITE; PS01186; EGF_1; 17.

PROSITE; PS01186; EGF_1; 17.

PROSITE; PS01186; EGF_2; 5.

PROSITE; PS01186; EGF_1; 17.

PROSITE; PS01186; EGF_2; 5.

PROFEMENTAIN, EGF_1; 17.

PROSITE; PS01186; EGF_2; 5.

PROFEMENTAIN, EGF_1; 17.

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LAMININ N-TERMINAL (DOMAIN VI).
LAMININ BGF-LIKE 1.
LAMININ BGF-LIKE 3.
LAMININ BGF-LIKE 3.
LAMININ BGF-LIKE 4.
LAMININ BGF-LIKE 5.
LAMININ BGF-LIKE 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 LNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSST 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 SLSLSKSKKGEVTFSPYSNSGAFSF-----SNAI-----LNGGSVSGLQRRDDTE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               457 GSVNNGEIN-----CLDNGSTYVIVEPVSGKGTVNIIS---GNLYLHYP 496
                                                                                                                                                                                                                                                                                                                                                                                                                                   SVSQSSSSASDVSSSVSQSSSSASDVSSSVSQSASSASD-----VSSSVSQSASSTSD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNAD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 VYGDLLVKKSKETYPGTEFDISGENFDVTGN--FNAEESAATSASIYSFTPSSFDNSGDI 411
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          SITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 VSSSVSQSSSASDVSSSVSQSSSSASDVSSSVSQSASSTSDVSSSVSQSASSTSGVSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSQSVSS----ASGSSSSFPQST-----SASTASGSATSNSLSSITSSASSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 ALSNSFIKK-----VIQNNEQSF---VG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATASNSLSSSDGTIYLPTTTISGDLTLTGKVIATEGVVVAAGAKLTLLDGDKYSFSADLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 TFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE---PSSRILANTNSITDVSWIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLA-GTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATST-
                                                                                                                                                                                                                             HYPOTHEFICAL PROTEIN YILL169C.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

F63E287A03F137EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                               6.4%; Score 128; DB 1; Length 995;
ilarity 16.1%; Pred. No. 5;
Conservative 100; Mismatches 152; Indels 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 106.1 kDa protein in GLY1-GDA1 intergenic region.
 Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    956 AA
                                                                                                                                         EMBL; 246921; canc...
SGD; S0001431; YIL169C.
InterPro; IPR004089; Chemotaxis_transducer.
InterPro; IPR000727; T_SNARE.
InterPro; inrotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            497 DIFTGQTVVFKGEGVLAVDPTETNATPIPVVGY 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SSNENNADKIP--GY
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                                                                                                                                                                                                                                              28
35
468
664
99735 MW;
                                                                                                                                                                                                                                                                                                                                                 ) 6.4%;
Similarity 16.1%;
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Best Local Simi
Matches 73;
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P32618;
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YEF3_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNGP-----ERITSDKYVADGRWYQAVVDRMGPNAKLTIREELPNGD-----VVEHS 2792
                                                                                                                                                                                                                                                                                                                                                                             ANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIR-----NNLVDLYNKA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                   SSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNADALSNSFIKKVIQNNEQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 ANNTTANPTPAVDEIKVAKIVLSGL-----RFGQN---TIELSVPTGEGNMNKVAPMI 368
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                    TDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNATLEQLKMAKTNLESAINQ-- 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamiyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PSTILELKTPEKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2612 VSQANKOLDDVEGSV-----SKLNELAEDIEEQQHRVGSQSRQLGQEI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 YSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                           Length 3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 99.7 kDa protein in SDL1 5'region precursor.
YIL169C OR Y19402.07C.
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                          ; Score 128.5; DB 1;
; Pred. No. 24;
48; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      995 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 GNIYLSSNEN--NADK----IPGYRRPG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
 6.48;
                                                                                                                                                                                                                                                                          23.48;
                                                                                                                                                                                                                                                                    Best Local Similaring watches 91; Conservative
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                                                     1463
1480
1487
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1896
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Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo I Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Cherry davides E., Bernen A., Brennan E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh (Petel F.X., Roberts D., Schl P., Schramm S., Shogren T., Smith Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;

Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                     Komp C.,
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                                                                  Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., F
Wel Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases
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MEDLINE-97148176; Pubmed-8994808;
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InterPro; IPR003961; FN_III.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
Hypothetical protein.
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Terashima H., Yabuki N., Arisawa M., Hamada K., Kitada K.;
Terashima H., Yabuki N., Arisawa M., Hamada K., Kitada K.;
"Up-regulation of genes encoding glycosylphosphatidylinositol
(GPI) attached proteins in response to cell wall damage caused by
disruption of FKS1 in Saccharonyces cerevisiae.";
Mol. Gen. Genet. 264-74(2000)
-- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR AND
SECRETED BY REGENERATING PROTOPLASTS.
-- SIMILARITY: BELONGS TO THE SPS2 FAMILY.
                                                                                                                                                                                                                                            730 QTSNATNTNPMHPQSLLAATLNDPSLQSFVRSGSFYSAPQPANSLQNNINGNETENISPR 789
--PSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQ 309
                                                                                 678 KGFTTDELDNYWTKQQPQVRSTNESLFSTTGTPMSSYK-----ANPVISPY--SSSHLR 729
                                                                                                                                                                   --GONTIELS-- 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                          ----VPTGEGNMNKVAPMIGNIYLSSNENNADKI 383
                                                                                                                                                                                                                                                                                                                                                                                                                   790 ISSDFNLLVPNLSPRLSNDVPIVPGNNTTLTPSHSNILTMNHQPTADNI 838
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
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COMPLUYEAST-2DPAGE; Q12355; --
Glycoprotein; Membrane; GPI-archor; Signal.
SIGNAL 1 19 POTENTIAL.
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PST1 OR YDR055W OR D4214 OR YD9609.09.
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MEDLINE=99251092; Pubmed=10234784;
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                                                                                                                                                                                                                  PTM: MEROZÓITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDa, 42 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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                                                                                                                Pan W., Tolle R., Bujard H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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Plasmodium falciparum merozoites: studies at the genetic level."; \rm EMBO~J.~4:3823-3829(1985).
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Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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10.7%; Pred. No. 11;
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InterPro; IPR000561; EGF-like.
                                                                                      REVISIONS, SEQUENCE FROM N.A.
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TSFAADSLESITDSLNLQSLTILT------SASFGSLQSVDSIKLITLPAISSFT 136
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     PROTOPLAST SECRETED PROTEIN 1. REMOVED IN MATURE FORM (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.3%; Score 126.5; DB 1; Length 444; 18.1%; Pred. No. 2.3;
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NCBI_TaxID=5839;
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230F60CACA5921A4 CRC64;
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(POTENTIAL) (POTENTIAL) (POTENTIAL) 19;

Gaps

Indels 113;

---SNSFIK 190

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID: MEROZOTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOTTES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                    13-AUG-1987 (Rel. 05, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
Marozolite Surface protein 1 precursor (Marozolite surface antigens)
(PMMSA) (P195).
                                                                                                                                                                                                                                                                                                                                                                                                   Holder A.A.;
Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
327 TPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADK 382
               (POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                              "Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites.";
Nature 317:270-273(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                        Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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MEROZOITE SURFACE PROTEIN 1.
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Pfam; PF00008; EGF; 1.
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MSP1_PLAFW
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Gaps

Indels 113;

Length 1639;

6.3%; Score 126.5; DB 1; 20.7%; Pred. No. 11; tive 62; Mismatches 155;

Conservative

Query Match Best Local Similarity 2

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242
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                                                   91 FDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLN 150
                                                                   151 GG----TLLDSN-EITTANKNINNTLSTINEQKTNADAL------SNSFIK 190
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               LASLQDYAK----IEASLSSAYSEAETVNNNLNATLEQLKMAKTNLESAINQANTDKTT 90
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Search completed: June 12, 2002, 10:51:05 Job time: 203 sec

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Q9f2d8 salmonella
O94358 schizosacch
Q9y7e9 candida gla
                mycoplasma
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MEDLINE-24025893: PubMed-8212828;
Saito S., Fujisawa A., Ohkawa S., Nishimura N., Abe T., Kodama K.,
Ramogawa K., Aoyama S., Iritani Y., Hayashi Y.;
Fiolining and DNA sequence of a 29 kilodalton polypeptide gene of
Mycoplasma galliseptium as a possible protective antigen.";
Vaccine 11:1061-1066(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2096;
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271 AA; 29817 MW; 8B25DE0CD5C85CA2 CRC64;
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SEQUENCE 271 AA; 29817
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99xh113 mycoplasma

99xh114 mycoplasma

949498 mycoplasma

92xid1 mycoplasma

92xid1 mycoplasma

94497 mycoplasma

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944467 mycoplasma

98xh15 mycoplasma

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                          Compugen Ltd.
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Copyright (c) 1993 - 2000 Comp
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sp_unclassified:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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Maximum Match 100%
Listing first 45 su
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sp_bacteriap:*
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sp_bacteria:*
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Maximum DB seq length: 200000000
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sp_plant:*
sp_rodent:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTP----VNYKYARRTVWN 237
                                                                                                                                                                                                                                                                                                                                                                                                                       62 NENATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 SDNGRISLISSTSDNSSTLTEVSWIYSLSGAGTKYSLIFNYGPSTGYLYFPYKLVKEGD
                              181 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE
                                         40;
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Phart G.T., Branton S.L., Hanson L.A., Minion F.C., Lott B.D., May J.D., Hughlett M.B.;
"A novel pMGA-like gene from the F-strain (vaccine strain) of
                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
PMGA-LIKE PROTEIN 9.2.
Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                    Length 671;
                                                                                                                                                                                                                                                                                                                                                                                         75; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                           Mycoplasma gallisepticum.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF210770; AAF25524.1;
SEQUENCE 671 AA; 71898 MW; 4D6AE6B59175D679 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 43.4%; Pred. No. 1.1e-33;
Matches 179; Conservative 75; Mismatches 118
                                                                                                                                              671 AA
                                                                                                                                              PRT;
                                                                                                                                                                                                                             Mycoplasmataceae; Mycoplasma
NCBI_TaxID=2096;
                                                                                                                                               PRELIMINARY;
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267 PSSRI 271
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366 SSDSDKVALEYKLNESAVKTIDFSPSQTSPVASDATRENNRSTAAPAQGSTEINPAPTLD 425
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                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 AADANNVGLQYKLNNGNVQQVEFATS-----TSANN-----TTANPTPAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHFATIKTNLTALYQSGKDIVTKTLDPLM-GTAINLSAVSQANTNISNAVSKLETWKTNA
                                                                                                                                                                                                                                                                                                                                                                                        39:
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NCBI_TaxID=29560;
                                                                                                                                                                                                                                                                                                                                                        41.6%; Score 831.5; DB 2; Length 702;
42.0%; Pred. No. 2.1e-33;
tive 84; Mismatches 116; Indels 39.
                                                                      rmorphyma gallisepticum.
Mycoplasma gallisepticum.
Mycoplasma group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 EIKVAKIVLSGLRFGQNTIELSVP-TGEGNMNKVAPMIGNIYLSSNENNADK
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B70AC874FE85055C CRC64;
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Last sequence update)
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 Created)
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75517 MW;
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                                                                                         Bacteria; Firmicutes; Bacillu
Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, VLHA1 PRECURSOR (FRAGMENT).
01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, PMGA1.4 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                            Matches 173; Conservative
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                                                                                                                                                                                                                                                                                                                    702 AA;
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Best Local Similarity
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                        NCBI_TaxID=2096;
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01-NOV-1999
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Gaps

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425 AVNNEMNPTPTVSDINIAKVTLSGLTFGENTIEFSVPT----NKVAPMIGNMYLTSNSG 479
                                                                                                                            69 NPNSGNTTPEQQLAAARKTLTDLLGTENTNVALYADYAKIQSTLSTAYMTAKTASENTSA 128
                                                                                                                                                                                             TLEQLKMAKINLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYN 125
                                                                                                                                                                                                                       235 VWNGD----EPSSRILANTNSITDVSWIYSLAGINTKYQFSFSNYGPSTGYLYFPYKLVKA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 ANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNEN 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NNINATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
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                                                                                                  10 NPNNGQT----QLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNLNA 65
                                                                                                                                                                                                                                                                                      126 QIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNADALS
                                                                                                                                                                                                                                                                                                              186 NSFIKKVIQNNEQSFVGTFTNAN--VQPSNYSFVAFSADVTP-----VNYKYARRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 ADSSSVALQYSLNKTSSKLINFEPAKTMPTNADQSENGVATTSTTEGRSSSEVLVADEVA
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STRAIN-HS;
STRAIN-HS;
Shen O.C., Bi D.R., Weng C.J.;
Shen O.C., Bi D.R., Weng C.J.;
Sequence analysis of the pMGA multigene family of Mycoplasma gallisepticum strain HS ";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275312; AAP391414.1; -.
SEQUENCE 680 AA; 72909 MW; A2ABC6500E3DFE47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
         Length 584;
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         40.3%; Score 805; DB 2; Length 58.
42.4%; Pred. No. 3.4e-32;
ive 72; Mismatches 113; Indels
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                                 Best Local Similarity 42.49
Matches 180; Conservative
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           Query Match
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                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 --VNYKYARRTVWNGDEPS---SRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTNADALSNSFIKKVIQNNEQSFVGTFTN----ANVQPSNYSFVAFSADVTP-----
MEDLINE-99392472; PubMed-10463176;
Markham P.F., Duffy M.F., Glew M.D., Browning G.F.;
"A gene family in Mycoplasma imitans closely related to the pMGA family of Mycoplasma gallisepticum.";
Microbiology 145:2095-2103(1999).
EMBL; AF141940; AAD39483.1; -.
                                                                                                                                                                                                                                                                                                                                                         36;
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Sequence analysis of the pMGA multigene family of Mycoplasma gallisepticum strain HS.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275312; AAF91415.1; -
Interpro; IPR001986; EPSP_SYNTASSe.
PROSITE; PS00104; EPSP_SYNTHASSE_1; UNKNOWN_1.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
NCBI_TaxID-2096;
                                                                                                                                                                                                                                                                                                              Length 632;
                                                                                                                                                                                                                                                                                                           Query Match 41.3%; Score 826; DB 2; Length 63
Best Local Similarity 45.3%; Pred. No. 3.4e-33;
Matches 183; Conservative 65; Mismatches 120; Indels
                                                                                                                                                                                                                               173F5B12E705BE47 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                           66959 MW;
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                                                                                                                                                                                                                                        632 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 DANPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                 :::| || || || : : : | SSSVALQYSLNKTSSKLINFKPAETVSTNTDQSENEVATTSTTEARSSYKVLVADEAATS 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 DNSSSTTQNLNEAKTRLETAIRTAATSKQTFDEQHAELVKVYEELKTTLSNETATLAPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 INADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 ARRIVW-NGDEPSSRILANT-----NSIIDVSWIYSLAGINTKYQFSFSNYGPSTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PG31, ATC19610;
STRAIN-PG31, ATC19610;
STRAIN-PG31, ATC19610;
STRDINRS-99003182: PubMed-9784576;
Liu L., Payne D.M., van Santen V.L., Dybvig K., Panangala V.S.;
Liu L., Payne D.M., van Santen V.L., Dybvig K., Panangala V.S.;
"A protein (M9) associated with monoclonal antibody-mediated
"A protein (M9) associated with monoclonal antibody-mediated
agglutination of Mycoplasma gallisepticum is a member of the pMGA
family.";
Infect. Immun. 66:5570-5575(1998).
                                                                       NTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Fírmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma, NCBL_TaxID=2096;
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SEQUENCE 645 AA; 69876 MW; 5A2F29572CFAE055 CRC64;
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Last annotation update)
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Best Local Similarity 42.3%; Pred. No. 2.9e-29;
Matches 172; Conservative 64; Mismatches 123
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294 ANNVGLQYKLNNGNVQQVEF----
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01-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 TLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIRNNLVDLYNKASSLITKTLDPLNG--GTLLDSNEITTANKNINNTLS--TINEQKTNA 181
                                                                                                                                                                                                            TVWTADSRIWTSPLPNNLQNSAPLTDVSWIYTLSGTGAKYTLTFDYYGPQTGYLYFPYKL 353
                                                                                                                                                                                                                                                     VKAADANNVGLQYKLNNGNVQQVEF------330
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VKTSD--KVGLQYKLNQADPVAIQFSEAAATASAPAETDGRQESAETATANEKVNPMPSV
                         INEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARR
                                                                                                                                                                       TVWNGD-----EPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKL
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                                                                                                                                                                                                                                                                                                                                       Mycoplasma gallisepticum.
Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
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        STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL---
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273E8915FEE57B9F CRC64;
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41.6%; Pred. No. 1.3e-29;
tive 62; Mismatches 127;
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75537 MW;
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Matches 176; Conservative
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                  MEDLINE-95010739; PubMed-7925999;
Markham P.F., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D.,
Browning G.F., Whithear K.G., Walker I.D.,
Browning G.F., Whithear K.G., Walker I.D.,
The organisation of the multigene family which encodes the major
surface protein, pMGA, of Mycoplasma gallisepticum.";
FEBS Lett. 352:347-352(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 QYAGIKMHLSGLYDAGKAITTKTLEPVEGDP-LTAGAVTMANTKIVEAIKDEVLNPKKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ADALSNSFIKKVİQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 RIVW-NGDEPSSRILANT-----NSITDVSWIYSLAGINTKYQFSFSNYGPSTGYLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 FPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTAN-PTPAVDEIKVAKIVLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 650;
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                                                                                                                                                                                                     STRAIN=S6;
Markham P.F.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                    HAEMAGGLUTININ.
3ABACDB65940EBBB CRC64;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403 LIFGSNKIEFSVPA----EKVSPMIGNMYLSSSPNNWNKI 438
                                                                                                                                                                                                                                                                                                                                                                                                                          37.2%; Score 744; DB 2; Le
42.9%; Pred. No. 3.7e-29;
ive 62; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 LRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI
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                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                             25 PC
650 HA
70249 MW;
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NCBI_TaxID=2096;
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                                                                                                                                                                                                                                                                      EMBL; U90714; AAB50152.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 42.9
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma gallisepticum.
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26 6
650 AA;
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01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSA----NNTTANPTPAVDEIKVA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DANPINGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                                                                                                                                                                                                                                                                                                                                Liu L., Payne D.M., van Santen V.L., Dybvig K., Panangala V.S.; A protein (M9) associated with monoclonal antibody-mediated agglutination of Mycoplasma gallisepticum is a member of the pMGA family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNADALSNSF1KKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARRIVW-NGDEPSSRILANT-----NSITDVSWIYSLAGTNTKYQFSFSNYGPSTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                  Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337 KIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l protein.
644 AA; 69866 MW; 8B9F352B13FBDE5C CRC64;
                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HYPOTHERICAL 69.9 KDA PROTEIN.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.3%; Score 745; DB 2; 42.3%; Pred. No. 3.3e-29;
                       644 AA
                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   Infect. Immun. 66:5570-5575(1998).
EMBL: AF053978; AAC69274.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-PG31, ATCC19610;
MEDLINE-99003182; Pubmed-9784576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2096;
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01-NOV-1996 (TrEMBLEEL: 01,
01-NOV-1996 (TrEMBLEEL: 01,
01-NOV-1998 (TrEMBLEEL: 08,
HAEMAGGLUTININ PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 172; Conservative
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                    PRELIMINARY;
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SEQUENCE FROM N.A.
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                    Q9ZHR9
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049495
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Q9ZHR9
                                         RNX OCC ON BRY
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232

342

346

283

cell

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Gaps

SEQUENCE

Signal.

RE DR KW KW SO SO

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NYKYARRTVWNGDEPSSRILANTNS-----ITDVSWIYSLAGINTKYQFSFSNYGPS 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 ENATKLADSLLSSIVKKITGVEE-----AHNKAQPANYSFVGYKRWYTELLLDKQVFP 279
                                                                                                                                                                                                                                                                                     STGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSA----NNTTANPTPAVDE 332
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                                                                                                                                                                                                                                               NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS
                                                                121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK
                                                                                                                                                                                                                            NYKYARRTVW-NGDEPSSRILLANT-----NSITDVSWIYSLAGTNTKYQFSFSNYGP
                                                                                                                                                                  TN----ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of the pMGA multigene family of Mycoplasma "Sequence analysis of the pMGA multigene family of Mycoplasma gallisepticum strain HS.";
Submitted (JUN-2000) to HE EMBL/GenBank/DDBJ databases.
EMBL; AF275312; AAF91413.1; -.
SEQUENCE 656 AA; 70875 MW; 58EA7E075FC617E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2096;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.2%; Score 704; DB 2; Length 656; Best Local Similarity 41.0%; Pred. No. 3.4e-27; Matches 166; Conservative 67; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Q9KH15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSA----NNTTANPTPAVDEIKVA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DANPNNGQ------TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                                                                                                                                                                                                                                                                                                                   NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                                                                                                                                         pMGA,
                                                                                                                                                                                              DANPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                                                                                                                                                                                                                                                                                                                                                                                                                     ARRIVW-NGDEPSSRILANT-----NSITDVSWIYSLAGINTKYQFSFSNYGPSTGY
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                                                                                                                                                                                                                                                                                                                                                            179 TNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKY
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-93162830; PubMed-8432610;
Markham P.F., Glew M.D., Whithear K.G., Walker I.D.;
MAlecular clothing of a member of the gene family that encodes lemagglutinin of Mycoplasma gallisepticum.";
Infect. Immun. 61:903-909(1993).
EMBL; M83178; AAR029651; -.
EMBL; S55216; AAB25397.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
                                                                                                                                                    48;
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                                                                                                                      Length 649;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.7%; Score 713; DB 2; Length 41.1%; Pred. No. 1.2e-27;
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33916673BB9E28C4 CRC64;
                                                             POTENTIAL.
356554BD2C72C1F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                    Score 743; DB 2; L
Pred. No. 4.1e-29;
62; Mismatches 125;
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70205 MW;
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               FEBS Lett. 352:347-352(1994).
EMBL; L28424; AAA62416.1; -.
                                                                                                                       Query Match 37.2%;
Best Local Similarity 42.3%;
Matches 172; Conservative 6
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Search completed: June 12, 2002, 10:50:40 Job time: 203 sec
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Best Local Similarity 40.1%;
Matches 149; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     Markham P.F., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D., Browning G.F., Whithear K.G., Walker I.D.; "The organisation of the multigene family which encodes the major surface protein, pMGA, of Mycoplasma gallisepticum."; FEBS Lett. 352:347-352(1994).
33 AMTLASLQDYAKIEASLSSAYSEAETVNNNLNATLEQLKMAKTNLESAINQANTDKTTFD
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U90714; AAB50154.1; -
InterPro; IPR002819; HD.
SEQUENCE 703 AA; 75742 MW; 310B69BE9F73CBC5 CRC64;
                                                                                                       338 IVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADK 382
                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04,
01-JUL-1997 (TrEMBLrel. 04,
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity
Matches 167; Conserv
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                          --GPAASVDNINVAKVNLANLNFGENTIEFSVP----MNKVAPMIGNMYITSDVAN
323 TANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=F;
Pharr G.T., Branton S.L., Hanson L.A., Minion F.C., Lott B.D.,
May J.D., Hughlett M.B.;
"A novel pMGA-like gene from the F-strain (vaccine strain) of
                                                                                                                                                                                                                                                                                                                                                             Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210770; AAF29525.1; -.
NON.TER 419 419
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2000 (TrEMBLrel. 15, Last annotation update)
PMGA-LIKE PROTEIN 9.3 (FRAGMENT).
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40.1%; Pred. No. 2.9e-23;
ive 58; Mismatches 122;
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785.975 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Abraham Marak alam	Hybrid Marek's dis	Mycoplasma qallise	Mycoplasma gallise	Mycoplasma gallise	Mycoplasma gallise	Mycoplasma gallise	Amino acid sequenc	MG-1 antiqen. AA	TMG-1 antigen. A	M.gallisepticum 26
	ID		AAW36051	AAR63230	AAR63229	AAR44493	AAR63227	AAR76955	AAP93646	AAR05081	AAR05082	AAR79911
	DB	181	18	15	15	14	15	16	10	11	11	16
	Query Match Length DB I	456	1086	615	610	368	368	368	235	235	261	261
æ	Query Match	100 0	99.8	95.3	95.6	80.4	80.4	80.0	57.0	57.0	57.0	57.0
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97WO-JP01084 96JP-0103548

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Fusion protein comprising herpes virus outer membrane protein and antigenic polypeptide – for prevention of infection by Mycoplasma gallisepticum, especially in poultry
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                                                                                                                 (JAPG ) NIPPON ZEON KK
                                                                                                                                          Tsuzaki Y,
                                                                                                                                                                    WPI; 1997-503046/46.
                                                                                                                                                                                N-PSDB; AAT96596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marek's disease virus; outer membrane protein; fusion protein;
                                                                                                               This sequence represents the chimeric protein 40 K-S which comprises a fragment of the Marek's disease virus outer membrane protein gB fused to an antigenic protein from Mycoplasma gallisepticum. The chimeric protein can be used in recombinant live vaccines for prevention of infection by Mycoplasma gallisepticum, especially as the outer membrane protein shows antigenicity in poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..672
/note= "derived from Marek's disease virus gB protein"
                                                                                                                                                                                                                                                                                                                   NNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGL 120
                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                    1 GCMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETV 60
                                                                                                                                                                                                                                                                                                                                                                    EPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGD
                                      Fusion protein comprising herpes virus outer membrane protein and antigenic polypeptide – for prevention of infection by Mycoplasma
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  693..1086
/note= "derived from M. gallisepticum antigen"
                                                                                                                                                                                                                                                  Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hybrid Marek's disease virus/M. gallisepticum 40 K-C protein.
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                 DB 18;
                                                                                                                                                                                                                                                Score 2004; DB 18;
Pred. No. 1.3e-128;
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Marek's disease gammaherpesvirus.
- Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMNKVAPMIGNIYLSSNENNADKIPGYRRPGTFL 394
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 16-19; 51pp; Japanese.
                                                            gallisepticum, especially in poultry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW36051 standard; Protein; 1086 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                100.0%; Sc
100.0%; Pr
tive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              poultry
                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 394; Conservative
WPI; 1997-503046/46.
N-PSDB; AAT96595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen; vaccine;
                                                                                                                                                                                                            456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric
Chimeric
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW36051
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This sequence represents the chimeric protein 40 K-C which comprises a fragment of the Marek's disease virus outer membrane protein gB fused to an antigenic protein from Mycoplasma gallisepticum. The chimeric protein can be used in recombinant live vaccines for prevention of infection by Mycoplasma gallisepticum, especially as the outer membrane protein shows antigenicity in poultry.
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                                                                                                                                                                                                                                                                                                                                                                   NNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               nnlnatleglkmaktnlesaingantdkttfdnehpnlveaykalkttlegratnlegl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPSSRILLANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGL
                                                                                                                                                                                                                                                                                                                                          1 GCMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKT
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                                                                                                                                                                                                                                             Length 1086;
                                                                                                                                                                                                                                             Score 2000; DB 18;
Pred. No. 7.5e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                             99.88;
99.78;
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                                                                                                                                                                                                                                                                                             Matches 393; Conservative
                                                                                                                                                                          1086 AA;
                                                                                                                                                                                                                                                                      Local Similarity
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AAR63229 standard; Protein; 610 AA.
 387 mnkvapmigniylssnennadki 409
                                                                                                                                                                                                                                                                                                                                                               Saitos,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610 AA;
                                                                                                                                                                                                                                                                  31-MAR-1994;
                                                                                                                                                                                                                                                                                      31-MAR-1993;
30-SEP-1993;
                                                                                             23-JUN-1995
                                                                                                                                                                                                                         WO9423019-A
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                                                                                                                                                                                                                                                                                                                                                                Saeki S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                       AAR63229;
                                                                                                                                                                                         Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGN 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ
                                                                                                                                                                                                                                                                                               Recombinant avipox virus combining DNA encoding a polypeptide - exhibiting antigenicity of mycoplasma, useful for the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                      1..615
/note= "Trp residues correspond to TGA codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 615;
                     recombinant avipox virus; live vaccine; mycoplasma antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                  Ohsawa I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.3%; Score 1910; DB 15; 98.2%; Pred. No. 4.7e-122; ive 3; Mismatches 4;
                                                                                                                                                                                                                                   ŝ
Mycoplasma gallisepticum antigen (UM-67).
                                                                                                                                                                                                                                   Ohkawa
                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 87-91; 123pp; Japanese.
                                                             Location/Qualifiers
                                                                                                                                                                                                                                   Iritani Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNKVAPMIGNIYLSSNENNADKI 384
                                                                                                                                                                                                                                             Takahashi K;
                                                                                                                                                                   93JP-0074139.
93JP-0245625.
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                                                                                                                                                                                                  (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                       gallisepticum
                                                                                                                                                                                                                                   Funato H,
                                                                                                                                                                                                                                                                 WPI; 1994-333181/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 376; Conser
                                                                                                                                                                                                                                             Saitos,
                                                                                                                                                                                                                                                                                                                                                                                                                             615 AA;
                                                                                                                                                                                                                                                                                                                     of a live vaccine
                                                                                                                                                                                                                                                                            N-PSDB; AAQ77857.
                                                                                                                                                31-MAR-1994;
                                                                                                                                                                   31-MAR-1993;
                                                                                                      WO9423019-A
                                                                                                                          13-OCT-1994
                                          Mycoplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                              Saeki S,
                                                                       Protein
                                                                                                                                                                                                                                   Аоуата
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A restriction fragment of the insert of M.gallisepticum genomic clone pUM-66 containing an open reading frame was sequenced (AAQ77856). The ORF encodes an antigenit polypeptide (AAAR63229). A recombinant avipox virus comprising the coding sequence can be used as a live vaccine to protect against infection by Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNLNATLEQLKMAKINLESAINQANIDKTIFDNEHPNLVEAYKALKTILEQRAINLEGLS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant avipox virus combining DNA encoding a polypeptide - exhibiting antigenicity of mycoplasma, useful for the production of a live vaccine
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0
                                                                                                                                                                                                          1..610 /-
/note= "Trp residues correspond to TGA codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 610;
                                                                                            recombinant avipox virus; live vaccine; mycoplasma antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohsawa I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.6%; Score 1856; DB 15; 95.5%; Pred. No. 2.2e-118; iive 10; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohkawa
                                              Mycoplasma gallisepticum antigen (UM-66).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 78-81; 123pp; Japanese.
                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H, Iritani Y,
Takahashi K;
                                                                                                                                                                                                                                                                                                                                                                             94WO-JP00541
                                                                                                                                                                                                                                                                                                                                                                                                                       93JP-0074139
93JP-0245625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.5%,
Matches 365; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI & CO LID.
(first entry)
                                                                                                                                        Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Funato H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-333181/41.
N-PSDB; AAQ77856.
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AAR44493;

AAR44493

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                                                                                                                                                     PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The plasmid pUTTW-1P contains a sequence (the TTW-1 gene) coding for the 40kD antigen of Mycoplasma gallisepticum under the control of a synthetic promoter. A 1300 bp restriction fragment containing the promoter-ORF sequence was excised and was used in the construction of plasmid pNZ7929-R2. This in turn was involved in the construction of a recombinant avigox virus vector comprising the TTW-1 gene, DNA encoding the signal membrane anchor peptide from Newcastle Disease Virus haemagglutinin neuraminidase and FPV sequences. The recombinant avipox virus is useful as a live vaccine
                              STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN
                                             ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant avipox virus combining DNA encoding a polypeptide -exhibiting antigenicity of mycoplasma, useful for the production of a live vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant avipox virus; live vaccine; mycoplasma 40kD antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohsawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "corresponds to a NNN codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "corresponds to a NNN codon"
                                                                                                                                                                                                                                         302 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohkawa
                                                                                                                                                                                                                                                                                                                                                                                                                            gallisepticum 40kD antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 71-74; 123pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                               AAR63227 standard; Protein; 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-JP00541
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93JP-0245625
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(SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Funato H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-333181/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saitos,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ77854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma
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                                                                                                                                                                                                                                                                                                                                                                 AAR63227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saeki S,
                                                                147
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                     PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 301
                                                                                                    YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGN 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN~61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence coding for the 40kDa antigen was obtained by PCR amplification of M.gallisepticum genomic DNA. The antigen reacts with Mycoplasma-immune or Mycoplasma-infected serum and can be used as a vaccine to protect fowl from M.gallisepticum infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "corresponds to NNN codon in AAQ53419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "corresponds to NNN codon in AAQ53419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma gallisepticum antigen and DNA coding for it for vaccination of fowl against mycoplasma infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.4%; Score 1612; DB 14; 95.0%; Pred. No. 4.8e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.8e-102
6; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohkawa S,
                                                                                                                                                                                                                                                                                                                                                                                     Vaccine; mycoplasma infection; poultry; fowl.
                                                                                                                                                                                                                                                                                                                                                       Mycoplasma gallisepticum 40kD antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 23-26; 37pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aoyama S, Fujisawa A, Iritani Y,
                                                                                                                                                                                                                                                             Ä.
                                                                                                                                                                   AAR44493 standard; Protein; 368
                                                                                                                                                 MNKVAPMIGNIYLSSNENNADK 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93WO-JP00715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92JP-0138819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma gallisepticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-405837/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ53419
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-1992;
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                                                                                                                                                                                                                                                                                                                                                                                      267 pssrilantnsitdvsxiyslagtntkyqfsfsnygpstgylyfpyklvkaadannvglg 326
AAQ94711 encodes AAR76955 Mycoplasma gallisepticum antigenic protein TTM-1. TTM-1 can be used as a vaccine for M. gallisepticum infectious diseases in poultry, and as a diagnostic agent for M. gallisepticum.
                                                                                                                                   Gaps
                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This amino acid sequence of MG1 is encoded by M1 DNA and elicits an
                                                                                                                                                                                                                                                                                                                                  of Mycoplasma gallisepticum (MG1) polypeptide.
                                                                                                                                                                                                                                                                  STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN
                                                                                                                                                                                                                                                                                ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE
                                                                                                                                                                                                                                                                                                                                                                          PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ
                                                                                                                                                           2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aoyama
                                                                                                                                 ö
                                                                                                       Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iritani Y,
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antigenic proteins of Mycoplasma gallisepticum
                                                                                                         Score 1604; DB 16;
Pred. No. 1.7e-101;
7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                             302 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                          χ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Катодама
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma gallisepticum; Poultry vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (JAPG ) NIPPON ZEON KK.
(SHIO ) SHIONOGI SEIYAKU KABUSHIKI KAISHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig.1a; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yanagida N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235
                                                                                                       80.0%;
ilarity 94.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP93646 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma gallisepticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1989-358393/49
                                                                                                                       Best_Local Similarity
Matches 318; Conser
                                                                    368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAN92568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-1989;
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                                                                     Sequence
                                                                                                            Query Match
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                                                                                                                                                                                                                                                                              182 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 241
                                                                                                                                                                                                                                                                                                                                  PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 301
                                                                                                                                                                         NNINATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                                                              Gaps
                                                                                                                     2 CMSITKKDANPNNGQTQLEAARMELIDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                    A new antigenic protein which reacts with Mycoplasma gallisepticum is useful in a component vaccine for use against poultry infected with M. gallisepticum.
                                                                                                                                                                                                                                                                                             ö
                                                                   Length 368;
  to protect against infection by Mycoplasma gallisepticum
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      poultry; diagnosis; TTM-1.
                                                                    2; DB 15;
4.8e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma gallisepticum antigenic protein TTM-1.
                                                                                                                                                                                                                                                                                                                                                                                                     YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
                                                                    Score 1612; D
Pred. No. 4.8e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR76955 standard; Protein; 368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Figs 5-6; 33pp; Japanese.
                                                                   Query Match 80.4%;
Best Local Similarity 95.0%;
Matches 320; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigenic protein; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93JP-0213102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma gallisepticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 262
                               368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ94711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR76955;
                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                327
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AAR76955
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121

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NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS
                                                            STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN
                                                                                                                                ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 236
                                                                                                                                           WPI; 1990-169109/22.
N-PSDB; AAQ04687.
                                                                                                                                                                                                                                                                                                                                                                                       (JAPG ) NIPPON ZEON (SHIO ) SHIONOGI KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 AA;
                                                                                                                                                                                                                                                                 TMG-1 antigen
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antigen-antibody reaction with anti-MG poultry sera. It can be used as a vaccine to prevent and diagnose MG infection. Doseage is at least 1 micro gram vaccine / kg. No acute toxicity was noted with a dose of 5 mg / kg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding the protein can be inserted into an expression vector for the prodn. of MG-1 polypeptide which elicits an antigen-antibody reaction with anti-mycoplasma gallisepticum poultry sera. It may also be ligated to other DNA to produce fusion proteins with an N-terminal bacterial enzyme sequence.

See also AAR05081-2 and AAR06437-41.
                                                                                                                                                                                                         62 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                                                                                                                               181
                                                                                          Gaps
                                                                                                                       61
                                                                                                              2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                                                                             STAYNOIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEOKTN
                                                                                                                                                                                                                                               182 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 236
                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnostic and vaccine for poultry mycoplasma serum – utilises antigen protein of the disease and recombinant vector
                                                                      Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 235;
                                                                                          Indels
                                                                    Score 1142; DB 10;
Pred. No. 2.8e-70;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1142; DB 11;
Pred. No. 2.8e-70;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma gallisepticum; poultry; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           incorporated with its coding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig la; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                         AAR05081 standard; protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.0%;
97.0%;
                                                                     57.0%;
larity 97.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                (first entry)
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Matches 228; Conservative
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N-PSDB; AAQ04686.
                                                                               Best Local Similarity
Matches 228; Conser
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                                                                      Query Match
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DNA encoding the protein can be inserted into an expression vector for the prodn. of MG-1 polypeptide which elicits an antigen-antibody reaction with anti-mycoplasma gallisepticum poultry sera. It may also be ligated to other DNA to produce fusion proteins with an N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 cmsitkkdanpnnggtq1qaarmeltd1inakartlas1qdyakieas1ssayseaetvn 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnostic and vaccine for poultry mycoplasma serum - utilises antigen protein of the disease and recombinant vector incorporated with its coding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.0%; Score 1142; DB 11; 97.0%; Pred. No. 3.2e-70;
                                                                                                                                                                                                                            Mycoplasma gallisepticum; poultry; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacterial enzyme sequence.
See also AAR05081 and AAR06437-41.
AAR05082 standard; protein; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 2; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   89JP-0136343.
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                                                                                                               08-OCT-1990 (first entry)
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This AA sequence of TWG-1 is encoded by TW-1 base sequence. It has the same sequence as that of a polypeptide expressed in Mycoplasma agallisepticum in nature. When the corresponding DNA sequence is inserted into a recombinant vector used to transform a host the antigen protein produced can be used as a vaccine to prevent and diagnose MG infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antigenic proteins of Mycoplasma gallisepticum – useful as poultry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JAPG ) NIPPON ZEON KK; (SHIO) SHIONOGI SEIYAKU KABUSHIKI KAISHA
 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1117; DB 10
Pred. No. 1.6e-68;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yanagida N, Kamogawa K,
                                                                                                                                                                                                                                                              Mycoplasma gallisepticum; Poultry vaccine; ss;
                                                                                                                                                                                                                            Amino acid (AA) sequence of TMG-1 polypeptide.
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                                                                                                                     AAP93959 standard; protein; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.78;
96.28;
                                                                                                                                                                                                                                                                                                                                                                                                      89EP-0005441.
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                                                                                                                                                                                           (first entry)
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Matches 227; Conservative
                                                                                                                                                                                                                                                                                                 Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saito S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1989-358393/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1989;
                                                                                                                                                                                          .11-MAY-1990
                                                                                                                                                                                                                                                                                                                                 EP345021-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kodama K,
                                                                                                                                                       AAP93959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                  207
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                                                                                                        AAP93959
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                  206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 181
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                                                                                                                                                                                                                                                                                                               Detection; probe; primer; PCR; amplification; secretion; lung; avian chronic respiratory disease; respiratory tract; nasal cavity.
Detection of Mycoplasma gallisepticum - for the quick detection, i.e. within one day, of avian chronic respiratory diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16;
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Pred. No. 3.2e-70;
3; Mismatches 4;
                                                                                                                                                                                                                                                                             M.gallisepticum 261 amino acid protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 10-11; 11pp; Japanese.
                                                                                                                                                                         AA.
                                                                                                                                                                         standard; Protein; 261
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                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma gallisepticum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-347462/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT04076
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(SHIO ) SHIONOG
                                                                                                                                                                                                                                                                                                                                                                                                    JP07236498-A.
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                                                                                                                                                                                                                                          19-JUL-1996
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Matches 185; Conservative
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                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                            JP07236498-A
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                               AAR79910;
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                                                                                                                                                                                                                                                                                                                                                               A restriction fragment of the insert of M.gallisepticum genomic clone pUM-81 containing an open reading frame was sequenced (AAO/7853). The OFF encodes an antigenic polypeptide (AAR63226). A recombinant avipox virus comprising the coding sequence can be used as a live vaccine to protect against infection by Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 ANNVGLQYKLNNGNVQQVEF-----ATSTSAN--NTTANP-----TPAVDEIKVAKIV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 ntnpsdgggmmnaaakeladakaalttiingetanlasyedyakikseltsayetakavs 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 DANPNNGQTQLEAARMELTD-----LINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PSSRILLANTNSITDVSWIYSLAGTNTKYQFSFSNYG-PSTGYLYFPYKLVKAAD
                                                                                                                                                                                                                                                                                                          Recombinant avipox virus combining DNA encoding a polypeptide - exhibiting antigenicity of mycoplasma, useful for the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                               1..661
/note= "Trp residues correspond to TGA codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 806; DB 15; Length 661;
Pred. No. 8.8e-47;
2; Mismatches 123; Indels 6;
                                                             recombinant avipox virus; live vaccine; mycoplasma antigen.
                                                                                                                                                                                                                                                     Ohsawa I;
                                                                                                                                                                                                                                                     Iritani Y, Ohkawa S,
                                            gallisepticum antigen (UM-81).
                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 61-65; 123pp; Japanese.
                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
                                                                                                                                                                                                                                                              Saitos, Takahashi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.2%;
                                                                                                                                                                             94WO-JP00541
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93JP-0245625
                                                                                                                                                                                                                           (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 42.8
Matches 185; Conservative
                             (first entry)
                                                                                  Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                       Funato H,
                                                                                                                                                                                                                                                                                 WPI; 1994-333181/41.
N-PSDB; AAQ77853.
                                                                                                                                                                                                                                                                                                                                                                                                                           661 AA;
                                                                                                                                                                                                                                                                                                                               of a live vaccine
                                                                                                                                                                                               31-MAR-1993;
30-SEP-1993;
                                                                                                                                                                               31-MAR-1994;
                             23-JUN-1995
                                                                                                                                           WO9423019-A.
                                                                                                                                                             13-OCT-1994
                                                Mycoplasma
                                                                                                                                                                                                                                                        Aoyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                 Saeki S,
          AAR63226;
                                                                                                               Protein
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                        Detection; probe; primer; PCR; amplification; secretion; lung; avian chronic respiratory disease; respiratory tract; nasal cavity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detection of Mycoplasma gallisepticum - for the quick detection, i.e. within one day, of avian chronic respiratory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
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341 LSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSS------
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42.8%; Pred. No. 8.8e-47;
tive 62; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "encoded by TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded by TGA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M.gallisepticum 661 amino acid protein.
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                                                                                                                                                                                                                                                                                                                                         AAR79910 standard; Protein; 661
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(SHIO ) SHIONOGI & CO LTD.
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|snlkfnsntiefsvptg-
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N-PSDB; AAT04075.
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multivalent live vaccines, also new probes for detecting Mycoplasma
                        Disclosure; Fig 3; 81pp; English.
        and manipulating its genome
                                                                                                                                                    Similarity
                                                                                                                647 AA;
                                                                                                                                          Query Match
Best Local Simi.
Matches 169;
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Matches
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                                                    341 LSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSS--------NENN 380
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                                                                            STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 181
                                                                                                                ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 241
                                                                                                                                                    -----PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYG-PSTGYLYFPYKLVKAAD 294
       DANPNNGQTQLEAARMELTD-----LINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New promoter region from a Mycoplasma gallisepticum adhesin gene useful when coupled to foreign antigen gene, for prodn. of
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/label- Sig_peptide
/note= "the signal peptide shows homology '
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                                                                                                                                                                                                                                                                                                                                                                                                Adhesin; pMGA; mycoplasma; diagnosis; vaccine; vector; respiratory disease; poultry; haemagglutinin.
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456 ptavtvdllkgy 467
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10-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                 61
Adhesin pWGA1.2 (AAW11978) and adhesin pWGA1.3 fragment (AAW11979) are products of gene sequences (see also AAT51531) isolated from Mycoplasma gallisepticum. DNA constructs incorporating the promoter and/or signal sequences of the pWGA genes can be used in the prodn. of multivalent live vaccines. The signal peptide sequence is utilised where attachment of an exogenous antigen gene to the mycoplasma cell membrane is required.
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                                                                                                                                                                                                                                                                                                        Length 647;
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                                                                                                                                                                                                                                                                                                     35.6%; Score 713; DB 16; 41.1%; Pred. No. 1.9e-40;
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Job time: 387 sec
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APPLICANT: Obsawa, Ikuroh
APPLICANT: Funato, Hirono
APPLICANT: Funato, Hirono
APPLICANT: Irilani, Yoshikazu
APPLICANT: Arakahashi, Kiyoohito
APPLICANT: Takahashi, Kiyoohito
TITLE OF INVENTION: NEW POLYPEPTIDE, DNA ENCODING THE
TITLE OF INVENTION: POLYPEPTIDE, RECOMBINANT VECTOR BEARING THE DNA AND
TITLE OF INVENTION: AS USE THEREOF
TITLE OF INVENTION: AS USE THEREOF
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND
ADDRESSEE: NAUGHTON
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 25-SEP-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                    US-09-268-347-28

US-09-268-347-34

US-08-714-481-2

US-08-714-481-2

PCT-US95-06111-2

US-09-268-347-49

US-09-268-347-49

US-09-347-47

US-08-169-927-2

US-08-169-95-4

US-08-138-447A-15

US-08-13-467-4

US-08-13-467-4

US-08-913-942-4

US-09-377-155-33

US-09-977-155-33

US-09-977-155-33

US-09-977-155-33

US-09-977-155-33

US-09-977-155-33

US-09-977-158-33

US-09-977-158-33

US-09-977-158-33

US-09-977-158-33

US-09-68-974-33
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FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00541
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REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 950811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08525742 Patent No. 5871742
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Ohkawa, Setsuko
Saeki, Sakiko
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Saito,
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US-08-525-742-10
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June 12, 2002, 10:49:08; Search time 22.56 Seconds (without alignments) 426.582 Million cell updates/sec
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-525-742-4
US-08-525-742-4
US-08-525-742-2
US-08-523-742-2
US-09-421-868-2
US-09-541-724-24
US-09-541-724-30
US-09-541-724-30
US-09-268-347-34
US-09-268-347-34
US-09-268-347-30
US-08-923-992A-2
US-08-923-992A-2
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US-09-043-123-2
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US-08-728-470-2
US-08-617-697-2
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US-08-530-198-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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806 159 159 135 135 135 134 131 131 129

Score

8

Result

126.5 126.5

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302 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGN 361
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.6%; Score 1856; DB 2;
95.5%; Pred. No. 3.5e-128;
tive 10; Mismatches 7;
                                                     PELLING DATE: 25-SEP-1995
CLASSIFICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
CLASSIFICATION ATA
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
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Patent No. 5871742
GENERAL INFORMATION:
APPLICANT: Saito, Shuji
APPLICANT: Ohkawa, Setsuko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 MNKVAPMIGNIYLSSNENNADK 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 8:
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Funato, Hirono
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saeki, Sakiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.5%
Matches 365; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-525-742-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: ZUZ COST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
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APPLICANT:
APPLICANT:
APPLICANT:
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                 SOFTWARE:
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APPLICANT: Aritani, Yoshikazu
APPLICANT: Asyama, Shigemi
APPLICANT: Takahashi, Kiyoohito
APPLICANT: Takahashi, Kiyoohito
TITLE OF INVENTION: NEW POLYPEPTIDE, DNA ENCODING THE
TITLE OF INVENTION: RECOMBINANT VECTOR BEARING THE DNA AND
TITLE OF INVENTION: RECOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                             Length 615;
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                                                                                                                                                                                                                                                                                                                Score 1910; DB 2;
Pred. No. 3.9e-132;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08525742
Patent No. 5871742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Saito, Shuji
APPLICANT: Ohkawa, Setsuko
APPLICANT: Saeki, Sakiko
APPLICANT: Ohsawa, Ikuroh
APPLICANT: Funato, Hirono
                                                                                                                                                                                                                                                                                                                      95.3%;
98.2%;
                             TELEFAX: 202-8870357
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 98.2
Matches 376; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                 ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-08-525-742-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
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Best Local S
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302 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
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COUNTRY:

COMPUTER READALE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPATIBLE

COMPATIBLE

TOWNSHIP

TOWNSH
                                                                                                                                                                                                                                      Sequence 4, Application US/08185851A Patent No. 5489430
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TELEPHONE: 202-659-2930
TELEFAX: 202-887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.4%;
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Saito, Shuji
APPLICANT: Ohkawa, Setsuko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Theresa M. Stevens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-887-0357
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 320; Conserva
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STREET: 17
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                                                                                                                                                                                                       US-08-185-851A-4
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STATE:
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                  APPLICANT: Acyama, Shigemi
APPLICANT: Takahashi, Kiyochito
APPLICANT: Takahashi, Kiyochito
TITLE OF INVENTION: NEW POLVEPETIDE, DNA ENCODING THE
TITLE OF INVENTION: POLYPEPTIDE, ECCOMBINANT VECTOR BEARING THE DNA AND
TITLE OF INVENTION: AS USE THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND &
ADDRESSEE: NAUGHTON
STREET: 1725 K Street, Suite 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
CHARLY APPLICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1638; DB 2;
Pred. No. 1.6e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .6; Mismatches
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APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: JP 05-245625
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: PCT/JP94/00541
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20006
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: McLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 956
TELECOMMUNICATION:
TELEPHONE: 202-659-2930
Iritani, Yoshikazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.7%;
95.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 368 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 322; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                     Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                        CITY: W
STATE:
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APPLICANT: Ohkawa, Setsuko
APPLICANT: Fujisawa, Ayumi
APPLICANT: Iritani, Yoshikazu
APPLICANT: Aoyama, Shijemi
TITLE OF INVENTION: Poultry Mycoplasma Antigens, Gene
TITLE OF INVENTION: Thereof and Recombinant Vectors Containing the Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
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ADDRESSEE: Armstrong, Westerman, Hattori, McLeland &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1612; DB 1;
Pred. No. 1.3e-110;
6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 YKLNNGNVQQVEFATSTSANNTTANPTQQLMRLKLLK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1725 K Street, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Theresa M. Stevens-Smith
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: PO-8-A930918
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                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Mismatches 154; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                         ----- 380
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                                                                                         105 AKTGATLNEVNEAKTTLDAAIKKAASAKNDFDAQHGSLVEAYNNLKETLKEEKTNLDSLA 164
                                                                                                                                       122 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 181
                                                                                                                                                             182 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 241
                  : ||::|| : || || || || || || 45 NTNPSDGGGMMNAAAKELADAKAALTTLINGETANLASYEDYAKIKSELTSAYETAKAVS 104
 61
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DANPNNGQTQLEAARMELTD-----LINAKAMTLASLQDYAKIEASLSSAYSEAETVN
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APPLICANT: FOSLET, Timothy J.
APPLICANT: McDevitt, Danien L.
TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene FILE REPERENCE: 0544.105011
CURRENT APPLICATION NUMBER: US/08/293,728D
CURRENT FILING DATE: 1944-08-22
NUMBER OF SEQ ID NOS: 20
SSOFTWARE: Patentin Ver. 2.0
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Pred. No. 0
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Best Local Similarity 22.8%
Matches 96; Conservative
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                                 PSSRILANTNSITDVSWIYSLAGINTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND ADDRESSEE: NAUGHTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.30
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42.8%; Pred. No. 2.9e-51;
Live 62; Mismatches 123;
                                                                                                        302 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
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Takahashi, Kiyoohito
/ENTION: NEW POLYPEPTIDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               Sequence 2, Application US/08525742 Patent No. 5871742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: McLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 95.
TELECOMMUNICATION:
TELEPHONE: 202-659-2930
                                                                                                                                                                                                                                                                                                                       APPLICANT: Obsawa, Ikuroh
APPLICANT: Funato, Hirono
APPLICANT: Iritani, Yoshikazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  Saito, Shuji
Ohkawa, Setsuko
Saeki, Sakiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/J
FILING DATE: 31 PAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 661 amino acids
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: AOYama, Shige
APPLICANT: Takahashi, K
TITLE OF INVENTION: NEW
TITLE OF INVENTION: POLITITLE OF INVENTION: RECC
TITLE OF INVENTION: AS I
NUMBER OF SEQUENCES: SI
CORRESPONDENCE ADDRESS:
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185; Conserve
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                                                                                                                                                                                   RESULT 5
US-08-525-742-2
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APPLICANT:
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Best Local 9
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208 ANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAG-TN 266

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192 IRKQAQQPDKKEDAEVKVREELGKLFSSTKAGLDQEIQEHVKKETSSEENTQKVDEHYAN 251
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                                                                                                                                                                                                                                                                                                                                APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group B
TITLE OF INVENTION: Streptococcal Beta Antigens
CORRESPONDENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 ITKKDANPNNGQTQLEAARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AE 58
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Best Local Similarity 22.7%; Pred. No. 0.064;
Matches 84; Conservative 51; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
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APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   Sequence 8, Application US/08923992A Patent No. 6280738 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1098 amino acids
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MOLECULE TYPE: protein
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                                                                RESULT 8
US-08-923-992A-8
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STATE:
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---IMAGDQ----VLANGVIDSDGNVIYTFTDYVN 324
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Best Local Similarity 22.8%; Pred. No. 0.0011;
Matches 96; Conservative 57; Mismatches 154; Indels 114; Gaps
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APPLICANT: McDevitt, Damien L.
TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene FILE REFERENCE: 05344.105011
CORRENT APPLICATION NUMBER: US/09/421,868
CURRENT FILING DATE: 1999-10-19
PRIOR RPLICATION NUMBER: 08/293,728
PRIOR FILING DATE: 1994-08-22
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6177084
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292 AKVPP---
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                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/09268347
Patent No. 6335182
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOSSUROICE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VET. 2.0
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Haemophilus influenzae US-09-268-347-24
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LENGTH: 1002
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Fatent No. 6335182

GENERAL INFORMATION:

APPLICANT: LOOSMORCE, Sheena M.

TILLE OF INVERTION:

FILE REFERENCE: 1038-860

CURRENT APPLICATION NUMBER: US/09/268,347

CURRENT FILING DATE: 199-03-16

NUMBER OF SEQ ID NOS: 54

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 671 VSELKDSKNSILDALEHSLQDISMSSQKLGNGISSELIELQKDWKESYRQLVQELRSLYN 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            731 LOHTHEESQKELMYGVRNDIDALVKTCTTSLNDADIILSDYISDQKSKFESKQQDLIANI 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 YSFVAFSADVTPVNYKYARRTVWNG----DEPSSRILANTNSITDVSWIYSLA----- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 GINTKYQ-------PSFSNYGPSIGYLYFPYKLVKAADANNVGL--QYKLNNGNVQ 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   894 GVNLEVQTLDRLLQKVKEHSEDNTKEKHQQL---LDLLESLVGNNDNLIDSIKTPHTELQ 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 QVE----FATSTSANNTT----- 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            611 NGYFTLLNDFNASMEELLNTHSNQLLISMTKITEHFQSLDEALQSARSSCAVPNSSLDLI 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 LEQLKMAKTNLESAINQANTDKTTFDNEHPN----LVEAYKALKTT---LEQRATNLEG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKNINNTLSTINEQ-KINADAL----SNSFIKK---VIQNNEQSFVGTFTNANVQPSN 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 NGQ-TQLEAARMELTDLINAKA-MTLASL----QDYAKIEASLSSAYSEAETVNNNLNAT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEIT-------TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1073;
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                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 135.5; DB 4;
20.9%; Pred. No. 0.067;
Live 76; Mismatches 182;
APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 134;
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Matches 97; Conservative
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US-09-541-782-6
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LENGTH: 1004
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60 VNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL------VEAYKALKT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 NNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVAF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SADVIPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFS----N 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TKYNPSVEDVKFTVTAKSDSKTTLDFSDLL----TKYNPSVSDRISTN 487
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                                                                                                                                                                                                                                                                                                                                                                                    77; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4. Application US/08923992A
Patent No. 6280738
GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 HSKLKOVVEDFRKKFKTSEQVTPKKRVKRDLAANENNOOKI-----ELTVSPENI----
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  51; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                   Score 131.5; Di
Pred. No. 0.15;
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APPLICATION NUMBER: US 60/024,707
                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                 6.68; 22.88;
                                              TELEPHONE: (202) 371-2600 TELEFAX: (202) 371-2540 INFORBATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                LENGTH: 1164 amino acids
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 22.89
Matches 84; Conservative
                                                                                                                                                                        TYPE: amino acid
TYPOPOLOGY: linear
MOLECULE TYPE: protein
US-08-922-992A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 DEIKVAKIV 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Tal, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-1gA FC Binding Forms of the Group B TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                346 GKLAKTKVKLVSANGTNPVKISNVADGTENTDAVSFK--QLKALQD-KQVTLSASNAYAN 402
                                                                                                                                                                                                                                                       403 GGSDADGGKGIQTLSNGLN----FKFKSTDGELLNIKAENDTVTFTPKKGSVQVGDDGK 457
                                                                                                                                                                                                                                                                                                                                                         158 ATIODGAKTTTGLVEASELVDSLNKLGWKVGTGTDGTGVTDGTHTDTLVKSGDKVTLKAG 517
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                                                                                                  1 GCMSITKKDANPNNGQTQLEAARM----ELTDLINAKAMTLASLQDYAKIEASLSSAYSE 56
                                                                                                                                                                                                    57 A-----ETVNNNLNATLEQLKMAKTNLESAINQANTDKTTF------DN-- 94
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                   Pred. No. 0.079;
i; Mismatches 160; Indels 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
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ZIP: 20005

COMPUTER REAGABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
                                                                                                                                                                                                                                                                                                        95 ------EHPNLVEAYKAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08923992A
Patent No. 6280738
20,3%; Pic.
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                                           Conservative
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                   Best Local Similarity
Matches 100; Conserv
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TILLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
TILLE REFERENCE: 1038-606
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 48
LENGTH: 2048
                                                                                                                                                                                                                                                                                                                                        Query Match 6.5%; Score 131; DB 4; Length 1104;
Best Local Similarity 20.2%; Pred. No. 0.15;
Matches 85; Conservative 50; Mismatches 154; Indels 132; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 RKQAQQADKKEDAEVKVREELGKLFSSTKAGLDQQIQEHVKKETSSEENTQKVDEHYANS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 VNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL------VEAYKALKT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 NNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVAF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 SADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGINTKYQFS--FSNYGP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 STGYLYFPYKLVKAAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 IVLSGLRFGQN-TIELSVPTGEGNM------NKVAPMIGNIYLSSNENNADKI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 ITIKNLKLNQSQTVTLKAKDDSGNVVEKTFTITVQKKEEKQVPKTPEQKHSKTEQNVPQE 528
                                                                                                                                                                                                                                                                                                                                                                                                                        7 KKDANPNNGQTQLEA-ARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AET 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448 SV-----SDRISTNYKTN----
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Patent No. 6335182
GENERAL INFORMATION:
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESEMENT AND ABER: 32,893
REFERENCE/DOCKET NUMBER: 1438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2640
INFORMATION FOR SEQ ID NO: 4:
SEQUIENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Haemophilus influenzae US-09-268-347-48
                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-923-992A-4
                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                 59 TVNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLE 118
                                                                                                                                                                                                                                                                             344 AVN------VAQLEAVVKWAKERRITFQGD-DNSTDVKIGLDNTL----TIK 384
                                                                                                                                                                                                                                                                                                                                           119 GLSSTAYNQIRNNLVDLYNKA--SSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTIN 176
                                                                                                                                                                                                                                                                                                                                                                                              385 GGAET -- NALTDNNIGVVKEADNSGLKVKLAKTLNNLT---- EVNTTTLNATTTVKVGS 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 EQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457 -TGSQSTSKTVYGVNGVKFTNNAETTAAIGTTRITRDKIGFARDG-DVDEKQAPYLDKKQ 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             515 LKVGSVAI--TIDNG-IDAGNKKISNLAKGSSANDAVTIEQLKAAKPTLNAGAGISVTPT 571
                                                        Gaps
                                                                                                          5 ITKKDAN-----PNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 WNGDEPSSRILANTNSI--TDVSWIYSLAGTN--TKYQFSFSNYGPSTGYLYFPYKLVKA
                                                     92;
Length 2048;
Ouery Match 6.4%; Score 129; DB 4; Length 200
Best Local Similarity 21.2%; Pred. No. 0.49;
Matches 83; Conservative 60; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: USA

ZIP: 2005

ZIP: 2005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORFUTER: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |: ||:|
438 SSSTTAELLSDSL------TFTQPN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 ELSVPTGEGNMNKVAPMIGNIYLSSNENNAD 382
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08923992A
Patent No. 6280738
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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US-08-923-992A-6
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109 TLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNI 168
                                                                                                                                                                                                                                                                          169 NNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVAF 220
                                                                                                                                                                                                                                                                                                                                     360 HSKLKQVVEDFRKKFKTSEQVTPKKRVKRDLAANENNQQKI-----ELTVSPENI----- 409
                                                                                                                                                                                                                                                                                                                                                                          221 SADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFS----N 275
                                                                                                                                                                                                                                                                                                                                                                                               60 VNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL-------VEAYKALKT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                     276 YGPSTG---YLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANP-TPAV 331
                                                                                                      Indels 77; Gaps
                                                                                                                                  7 KKDANPNNGQTQLEA-ARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AET 59
                                                                       Query Match 6.3%; Score 126.5; DB 4; Length 1128; Best Local Similarity 22.5%; Pred. No. 0.33; Matches 83; Conservative 51; Mismatches 158; Indels 77;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-923-992A-6
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Search completed: June 12, 2002, 10:49:10 Job time: 203 sec

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139.5 7.0 2401 2 138.5 6.9 1314 1 137.5 6.9 820 2 137.5 6.9 926 2	34 137.5 6.9 989 2 D89852 35 137.5 6.9 1524 2 68553 36 137.5 6.9 4152 2 T31102 37 137 6.8 719 2 S55119 38 136.5 6.8 568 2 E97066	136.5 6.8 1073 2 136.5 6.8 2271 2 135.5 6.8 1085 2 135.5 6.8 1238 2	135 6.7 2269 2 134.5 6.7 589 2	ALIGNMENTS	ס מכנונים ו	S48754 (S48754 major surface protein (clone pMGA1.4) precursor	C.Species: Mycopiasma gailisepticum C.Date: Ul-Aug-1995 #sequence_revision 03-Nov-19 C.Accession: 848754 R.Markham, P.F.; Glew, M.D.; Sykes, J.E.; Bowden	FEBS LECT. 352, 347-352, 1994 A;Title: The organisation of the multigene famil A;Reference number: S48751; MUD:95010739 A;Accession: S48754 A;Status: preliminary; nucleic acid sequence not	A;Molecule type: DNA A;Residues: 1-702 <mar> A;Cross-references: EMBL:L28424</mar>	C;Genetics: A;Genetic code: SGC3 A;Start codon: GTG	Query Match 41.5%; Score 831.5;	3; Conservative 84; Mismatche	Oy 9 DANPNNGQTQLEAARMELTDLINAKAMTLASI 		Qy 63 NLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLV	Db 128 NTSATLEQVKSATSTLQTAIDTAASSKTSFDEKNPELI	Qy 123 TAXNQIRNNLVDLXNKASSLITKTLDPLNGGTLLDSNE	Db 188 SNFATIKTNLTALYQSGKDIVTKTLDPLM-GTAINLSA	QY 183 DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAF	r SFVKEVLVKNKLTG	QY 237 WNGDEPSSRILANTNSITDVSWIYSLAGINTKY	DD 306 WTSNIDILSQPQPAEGENQQSAPDVSWIYNLIGMGAKY	QY 292 AADANNVGLQYKLNNGNVQQVEFATSTSA	DD 366 SSDSDKVALEYKLNESAVKTIDFSPSQTSPVASDATRE	Qy 333 EIKVAKIVLSGLRFGQNTIELSVP-TGEGNMNKVAPMI	DD 426 DIKIAKVILSNLKFGSNTIEFSVPTTAKEGTSKVAPMI
GenCore version 4.5 : (c) 1993 - 2000 Compugen Ltd.	th, using sw model 2002, 10:49:47; Search time 29.99 Seconds (without alignments) 1262.394 Million cell updates/sec	-052-4_COPY_693_1086 :KDANPNNGQTQLESSNENNADKIPGYRRPGTFL 394	), Gapext 0.5	js, 96089334 residues	ying chosen parameters: 283138	200000000	Match 0% Match 100% first 45 summaries		her of results predicted by chance to have a	score of the result otal score distribut RIES	n na th	TOTAL TOTAL	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2 S48752 major surface 2 A49218 hemagglutinin	2 S48755 2 S51560	2 B89921 hypothetical p 1 JC6009 surface-locate	2 AG2422 2 D90011	2 C89921 hypothetical 2 S41539 fibrinogen-bi	2 B71605 2 A86827	2 F82885 hypothetical 2 C4/131	2 T30822 2 T30822 2 D71850	2 PC6003 surface membr	2 118351 2 H71879	2 AG2560 h 2 AC0976 P	2 140402 2 B49218 3 E05023	00 2 E85822 probable invasin 2 15 2 F95097 phage-related prot 14 2 D71917 toxin-like outer m
Copyright	OM protein - protein search, Run on: June 12, 20	Title: US-09-147-052-4_CO Perfect score: 2004 Sequence: 1 GCMSITKKDANPNNGQ	Scoring table: BLOSUM62 Gapop 10.0	Searched: 283138 seqs	Total number of hits satisfying	Minimum DB seq length: 0 Maximum DB seq length: 20000	Post-processing: Minimum Mat Maximum Mat Listing fir	Database : PIR_71:* 1: pirl:* 2: pir2:* 3: pir3:*	4: pir No. is the	e greater tha Is derived by	8 Result Query No Score Match Length	10000	831.5 41.5 754 37.6 744 37.1	743 37.1 713 35.6	575.5 28.7 189.5 9.5	175 8.7 173 8.6	0 165.5 8.3	2 163.5 8.2 3 159 7.9	4 156 7.8 5 155 7.7	5 155 7.7	8 154.5 7.7 9 151 5 7.7	151 7.5	145 7.2	3 144.5 7.2 4 144 7.2 5 143 6 7.3	6 142 7.1	27 142 7.1 2660 28 141.5 7.1 1645 29 140.5 7.0 3194

surfac ng, G.F

QY         237 WNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQESFSNYGPSTGYLYFPYKLVK 291           1         :   <t< th=""></t<>
QY 183 DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 236
123 TAYNOIRNNIVDLYNKASSLITKTLDPLNGGTLLDSNBITTANKNINNTLSTINEQKTNA :
63 NLNATLEQLKWAKTNLESAINOANTDKTTFDNEHPNIVEAYKALKTTLEQRATNLEGLSS  1 :
9 DANDNINGOTOLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNN
Juery Match  41.5%; Score 831.5; DB 2; Length 702;  42.0%; Pred. No. 3.6e-38;  42.0%; Pred. No. 3.6e-38;  42.0%; Pred. No. 3.6e-38;  42.0%; Pred. No. 3.6e-38;  43.0%; Pred. No. 3.6e-38;  44.0%; Pred. No. 3.6e-38;  45.0%; Pred. No. 3.6e-38;  46.0%; Pred. No. 3.6e-38;  47.0%; Pred. No. 3.6e-38;  48.0%; Pred. No. 3.6e-38;  49.0%; Pred. No. 3.6e-38;  49.0%; Pred. No. 3.6e-38;  40.0%; Pred. No. 3.6e-3

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A;Cross-references: GB:U90714; EMBL:L28423; NID:g1905869; PIDN:AAB50152.1; PID:g19058 R;Markham, P.F.; Glew, M.D.; Brandon, M.R.; Walker, I.D.; Whithear, K.G. Infect. Immun. 60, 3885-3891, 1992 A;Title: Characterization of a major hemagglutinin protein from Mycoplasma gallisepti A;Title: Characterization of a major hemagglutinin protein from Mycoplasma gallisepti A;Reference number: A44793; MUID:92363591 A;Contents: S6 A;Accession: A44793 A;U1D:92363591 A;Status: preliminary A;Molecule type: protein A;Residues: 26-42 <MA2> A;Note: sequence extracted from NCBI backbone (NCBIP:111017) C;Genetics: A;Genetic code: SGC3 A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 FPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTAN-PTPAVDEIKVAKIVLSG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::| :| || || ||:|| || || || :| || :| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| :| sssttonlneaktrletairtaatskotfdeohaelvkvykelktytlenetataepyada 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQKTN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTVW-NGDEPSSRILANT-----NSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLY 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKYAR
                                                                                                                                                                                                                                                                                                                                                                                                         11 NPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                 37.1%; Score 744; DB 2; Length 65
42.9%; Pred. No. 2e-33;
iive 62; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 LRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 384
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Best Local Similarity 42.3'
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.9%
Matches 172; Conservative
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A; Residues: 1-649 <MAR>
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A; Start codon: C
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                                                                                           C; Species: Mycoplasma gallisepticum
C; Species: Mycoplasma gallisepticum
C; Species: Mycoplasma gallisepticum
C; Species: Mycoplasma gallisepticum
C; Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999
C; Accession: $48753
R; Markham, P.F.; Glew, M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F.; PEBS Lett. 352, 347-352, 1994
A; Markham, P.F.; Glew, M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F.; PEBS Lett. 352, 347-352, 1994
A; Reference number: $48751; MUID:95010739
A; Recession: $48753
A; Recession: S48753
A; Residues: 1-702 <AMR>
A; Residues: 1-702 <AMR>
A; Residues: 1-702 <AMR>
A; Residues: EMBL:L28424; NID:9535687; PIDN:AAA62417.1; PID:9535690
C; Genetics: A; Genetic code: SGC3
A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 NPNNGQT----QLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTP-----VNYKYARRTVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 NGD--EPSSRILANIN-SITDVSWIYSLAGINTKYQFSFSNYGPSTGYLYFPYKLVKAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match

37.6%; Score 754; DB 2; Length 702;
Best Local Similarity 41.6%; Pred. No. 6.2e-34;
Matches 176; Conservative 62; Mismatches 127; Indels
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A;Residues: 1-650 <MAR>
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major surface protein (clone pMGA1.2) precursor - Mycoplasma gallisepticum major surface protein (clone pMGA1.2) precursor - Mycoplasma gallisepticum c; Species: Mycoplasma gallisepticum c; Species: Mycoplasma gallisepticum C; Date: Ol-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999 C; Accession: S48752 A; M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F. FEBS Lett. 352, 347-352, 1994 A; Title: The organisation of the multigene family which encodes the major cell surface A; Fitle: The organisation of the multigene family which encodes the major cell surface A; Accession: S48751; MUID:95010739 A; Accession: S48752 A; Accession: S48752 A; Accession: S48751 A; A; Status: precliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:L28424; NID:9535687; PIDN:AAA62416.1; PID:9535689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.1%; Score 743; DB 2; I
42.3%; Pred. No. 2.2e-33;
iive 62; Mismatches 125;
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A; Cross-references: EMBL:L28424; NID:9535687; PIDN:AAA62419.1; PID:9535692
A; Orde: the sequence of residues 385-386 and the corresponding nucleotide s C; Genetics:
A; Genetics: SGC3
A; Start codo: GTG
                 --NNTTANPTPAVDE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 NINATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 DANPING-----OTOLEAARMELTDLINAKAMTLASLODYAKIEASLSSAYSEAETVNN 62
                                       123 TA-YNQIRNNLVDLYNKASSLITKTLDPLN-GGTLLDSNEITTANKNINNTL--STINEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 KTNADALSNSFIKKVIQNNEQSFVG---TFTNANVQPSNYSFVAFSADVTP-----VNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 KYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGINTKYQFSFSNYGPS-TGYLYFPYK
                                                                                                      334 IKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.7%; Score 575.5; DB 2;
42.3%; Pred. No. 1.6e-24;
live 50; Mismatches 113;
                   STGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 LVKAADANNVGLQYKLNNGNVQQVEF 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 138; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hemagilutinin homolog pMGA1.2 - Mycoplasma gallisepticum
C;Species: Mycoplasma gallisepticum
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 07-Dec-1999
C;Accession: A49218
R;Markham, P. P.; Olew, M.D.; Whithear, K.G.; Walker, I.D.
Infect. Immun. 61, 903-909, 1993
A;Title: Molecular cloning of a member of the gene family that encodes pMGA, a hemagglut
A;Reference number: A49218; MUID:93162830
A;Status: preliminarv
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                                                                                                                                                                                                        TNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV------NYKY 231
                                                                                                                                                                                                                                                                          ARRIVW-NGDEPSSRILANT-----NSITDVSWIYSLAGINTKYQFSFSNYGPSTGY 282
                                                                                                                                                                                                                                                                                                                                             LYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSA----NNTTANPTPAVDEIKVA 337
                                                                                                                                                                                                                                                                                                                                                                  48 DINPGDGQGMMNAASQELAAARMGLTIFDSKAKNLGLYVDYKKTQNTLTKAYDAAKTVL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| ::| : | ||| ||-|| || || || || :| ||-|| ||-|| || :| ||-||| ||-||-|| DNSSSTTQNLNEAKTRLETAIRTAATSKQTFDEQHAELVKVYKELKTTLSNETATLAPYA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: sequence extracted from NCBI backbone (NCBIN:125182, NCBIP:125183)
9 DANPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 DANPNNG9-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:S55216; NID:g265625; PIDN:AAB25397.1; PID:g265626
A;Experimental source: S6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TN----ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.6%; Score 713; DB 2; Length 647; 41.1%; Pred. No. 9.6e-32; ive 60; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    KIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 384
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Matches 169; Conservative
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Molecule type: DNA; protein
Residues: 1-647 <MAR>
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C; Genetics:
A; Genetic code: SGC3
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                                                                                                                                    122
                                                                                                                                                                      168
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gene sys

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"Species: Anabaena sp. (strain pcc 7120) species: Anabaena sp. (strain pcc 7120) c; Species: Anabaena sp. (strain pcc 7120) is a synonym of Nostoc sp. strain pcc 7120 A; Note: Anabaena sp. (strain pcc 7120) is a synonym of Nostoc sp. strain pcc 7120 c; pate: 14-pec-2001 #sequence_revision 14-pec-2001 #text_change 11-Jan-2002 C; Accession: AG2422 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: surface-located membrane protein lmp3; tetratricopeptide repeat homolo C; Superfamily: surface-located membrane protein c; Superfamily: surface-located membrane protein Lmp3 #status predicted <SIG> F; 1-24 Domain: signal sequence #status predicted <SIG> F; 25-1302/Product: surface-located membrane protein Lmp3 #status predicted <MAT> F; 957-992/Domain: tetratricopeptide repeat homology <TT1> F; 993-1026/Domain: tetratricopeptide repeat homology <TT2> F; 1089-1120/Domain: tetratricopeptide repeat homology <TT3> F; 1154-1190/Domain: tetratricopeptide repeat homology <TT3> F; 1154-1190/Domain: tetratricopeptide repeat homology <TT4>
                                                                                                                                                                                                                                                                                                                         C; Accession: JC6009
R; Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G. B.; Bacteriol. 178, 2775-2784, 1996
A; Title: Analysis of 0.5-kibbase-pair repeats in the Mycoplasma hominis lmp A; Reference number: JC6009; MUID:96213016
A; Accession: JC6009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-1302 <LAD>
A;Cross-references: EMBL:X95601; NID:g1197335; PIDN:CAA64858.1; PID:g1197336
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NNNLNATLEQLKMAKTNLESAINQANTDKTTFDN-----EHPN-----LVEAYKAL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ITKKDANPNNGQ----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 KITLEQRAINLEGLSSTAYNQI-RNNLVDLYNKASSL-----ITKTLDPLNGGTLLDSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
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                                                                                                                                                                                                                                                surface-located membrane protein 1mp3 precursor - Mycoplasma hominis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 KIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNI--YLSSNENNADKIPGY 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
8.6%; Score 173; DB 1; Length 1302;
Best Local Similarity 22.8%; Pred. No. 0.08;
Matches 94; Conservative 67; Mismatches 163; Indels 8
-----KVAPMIGNIYLSSNEN 379
                                                                     886 LOGAINDKDATLRNONYLDADES 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: 1mp3
A;Genetic code: SGC3
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       364
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C; Species: Staphylococcus aureus
C; Species: Staphylococcus aureus
C; Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
C; Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
C; Accession: B89921
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R; Kuroda, M.; Ohta, T.; Wobayashi, N.; Sawano, T.; Inoue, R.; Katto, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Reference number: A89758; MUID:21311952; PMID:11418146
A; Scatus: preliminary
A; Molecule type: DNA
A; Residues: 1-6713 cKUR>
A; Cross-references: GB:BA000018; PID:g13701232; PIDN:BAB42527.1; GSPDB:GN00149
A; Cross-references: strain N315
C; Genetics:
A; Gene: ebhA
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K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADVIPVNYKYARRIVWNGDEPSSRILANTNSITDVSWIYSLA------GTNTKY 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 AYNQIRNNLVDLYNKAS-SLITKTLDPLNG--GTLLDSNEITTANKNINNTLSTINEQKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFS 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                              A.C.C.S.S.Teferences: EMBL:L28424; NID:g535687; PIDN:AAA62415.1; PID:g535688 C;Genetics: A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                       292 AADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTI 351
                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                        Length 320
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22.6%; Pred. No. 0.55;
Live 66; Mismatches 179; Indels
                                                                                                                                                                                                                                    Query Match
9.5%; Score 189.5; DB 2; Length
Best Local Similarity 48.9%; Pred. No. 0.0016;
Matches 46; Conservative 11; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELSVP-TGEGNMNKVAPMIGNIYLSSNENNADKI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELSVPTTDEEGTSKVAPMIGNMYITSNDQNQRKI 124
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Matches 100; Conservative
                       A; Residues: 1-320 <MAR>
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hypothetical protein ebhB [imported] - Staphylococcus aureus (strain N315)

C; Species: Staphylococcus aureus
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
C; Accession: G9921
C; Accession: G9921
C; Accession: G9921
C; Skuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; (ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, I. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 557, 1255-1240, 2001
Lancet 557, 1255-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Reference number: A89758; MUID:21311952; PMID:11418146
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A;Molecule type: DNA
A;Residues: 1-3890 <KUR>
A;Cross-references: GB:BA000018; PID:g13701233; PIDN:BAB42528.1; GSPDB:GN00149
A;Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1447 KANEQKAL------IAQTADATTEEKEQANQQVDAQLTQGN-QNIENAQSI 1490
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                                                                                                                                                                                                                                                                                                                                                   1303 NDQNATNEEKEAAIQQLATAVTDAKNNITAATDDNGVDTAKDAGKNSIQSTQP---ATAV 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1360 KSNAKNEVDQAVTTQNQAIDNTTGATTEEKNAAKDL-----VLKAKEKAYQDIL---N 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 TNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIRNNLVDL 135
                                                                                                                                                                                                                                                                                  111 -EQRATNLEGLS-----STAYNQIRNNL------VDLYNKASSLITKTLDPLNGGTLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                       157 DSN-----EITTANKNINNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTFTNAN 209
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                                                     9 DANPNNGQTQLE-----AARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAE
                                                                                                                                              59 TVNNNLN-----ATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 VQPSNYSFVAFSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLA----GT
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24.4%; Pred. No. 1.1;
ve 54; Mismatches 153;
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Best Local Similarity 24.4%
Matches 94; Conservative
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C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C; Accession: D90011
R; Kurodo, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                     Ana
              M.; Tabata,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium PA;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG242
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-661 < KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76634.1; PID:g17134073; GSPDB:GN00179
A;Cross-references: strain PCC 7120
C;Genetics: A;Genetics: A;Gen
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A,Residues: 1-2481 <KUR>
A;Cross-references: GB:BA000018; PID:g13701961; PIDN:BAB43253.1; GSPDB:GN00149
A;Experimental source: strain N315
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A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 NLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNADALSNSFI 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----NTALNTATNNF 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%; Score 165.5; DB 22.7%; Pred. No. 0.084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 MIGNIYLSSNENNADKIPGYRRPGTFL 394
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Matches 88; Conserv
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Best Local S:
Matches 98;
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R.Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh Genome Res. 11, 731-753, 2001
Affilte: The complete genome sequence of the lactic acid bacterium Lactococcus lacils A; Reference number: A86625; MUID:21235186; PMID:11337471
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A86827
hypothetical protein yqfG [imported] - Lactococcus lactis subsp. lactis (strain IL140
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: A86827
                                                                                                                                                                                                                                                                                                                                                                   A;cross-references: GB:AE001420; GB:AE001362; NID:g3845287; PIDN:AAC71959.1; PID:g384
A;Experimental source: clone 3D7
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: B71605
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71605
A;Reference number: B71605
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A;Molecule type: DNA
A;Residues: 1-1072 <STO>
A;Cross-references: GB:AE005176; PID:g12724625; PIDN:AAK05715.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
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                                                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 ---NNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVT
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21.0%; Pred. No. 0.6;
tive 76; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 156;
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Matches 97; Conservat
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Best Local Similarity
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A; Residues: 1-807 <GAR>
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746 NNLTTSN 752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibrinogen-binding protein - Staphylococcus aureus
Ni Alternate names: clumping factor
Cispecies: Staphylococcus aureus
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RimcDevitt, D.; Francois, P.; Vaudaux, P.; Foster, T.J.
Mol. Microbiol. 11, 233-248, 1994
A.7Title: Molecular characterization of the clumping factor (fibrinogen receptor) of Staphylococcus aureus aureus aureus
A.7Title: Molecular characterization of the clumping factor (fibrinogen receptor) of Staphylococcus aureus aureus aureus
A.7Title: Molecular characterization
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                     NNDKQTAYNNAVAAAETIINANSNPEMNPSTITQKAE--QVN---SSKTALNGDENLATA 3737
                                                                                 242 -PSSRILANT-NSITD-----VSWIYS---LAGTNTKYQFSFSNYGPSTGYLYFPYKLV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 MSITKKDANPNNGQTQL--EAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETV 60
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                                                                                                                                                                                                    291 KAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDE-IKVAKIVL---SGLRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STTQDTSTEATPSNNESAPQSTDASNKDVVNQAVNTSAPRMRAFSLAAVAADAPAAGTDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 933;
                                                                                                                   ::: || || || :| :| || 3738 KONAKTYLNTLTSITDAQKNNLISQISSATRVSGVDTVKQNA----
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0.3;
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                                                                                                                                                                                                                                                                                                                                                          3836 AQNAVEAALQRVNTAKDALNGDAKLI 3861
                                                                                                                                                                                                                                                                                                                       GONTIELS --- VPTGEGNMNKVAPMI 369
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Matches 96; Conserv
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Search completed: June 12, 2002, 10:49:50 Job time: 208 sec

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June 12, 2002, 10:51:05 ; Search time 17.44 Seconds (without alignments) 874.742 Million cell updates/sec
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2004
1. GCMSITKKDANPNNGQTQLE......SSNENNADKIPGYRRPGTFL 394
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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105224 Total number of hits satisfying chosen parameters:

105224 segs, 38719550 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	lactococ	P78586 c arg5,6 pr	saccharom		P24339 schizosacch	P47580 mycoplasma		_	_	Q00174 drosophila	P40442 saccharomyc	P32618 saccharomyc				P54674 dictyosteli			P14738 staphylococ	P40957 saccharomyc	P34231 saccharomyc	-	Q05870 schistosoma	-	Q09904 schizosacch		P04931 plasmodium	3 lactococ	90	_	386	690	P19880 saccharomyc
SUMMARIES	ID	ISF	AR56_CANAL	SW11_YEAST	YM41_YEAST	CUT7_SCHPO	X338_MYCGE	BAG_STRAG	RBP2_PLAVB	WAPA_BACSU	LMA_DROME	YIQ9_YEAST	YEF3_YEAST	PST1_YEAST	MSP1_PLAFK	MSP1_PLAFW .	P3K2_DICDI		YKK1_CAEEL	FNBA_STAAU	MAD1_YEAST	YKS7_YEAST	NSP1_YEAST	MYSP_SCHJA	YN96_YEAST	N124_SCHPO	CAT8_YEAST	ARP_PLAFA	P2P_LACLC	ALS1_CANAL	MRSP_STAAU	USO1_YEAST	- T	PDR4_YEAST
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PMPB_CHLMU YBYO_YEAST YMSG_YEAST TOMG_SALEN YSRA_CAEEL PIP_LACLA PIP_MYCHR KIPI_YEAST P2P_LACPA VP4_ROCPEH INNA_LISMO PAC_STRMU	O9pjy2 chlamydia m		Q04893 saccharomyc	Q54001 salmonella	Q09625 caenorhabdi	P49022 lactococcus	P41508 mycoplasma	P28742 saccharomyc	Q02470 lactobacill	Q02945 equine rota	P25146 listeria mo	P11657 streptococc
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	12	H										

## ALIGNMENTS

Candida albicans (Yeast). Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.

NCBI\_TaxID=5476;

Nombela C.; of the ARG5,6 gene of

SEQUENCE FROM N.A.
STRAIN-ATCC 64385 / 1001;
MEDLINE-97195775; PubMed-9043106;
Negrado A., Monteoliva L., Gil C., Pla J.,
"Cloning, analysis and one-step disruption
candida albicans.";

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                                                                                                                                                                                                                                                                                                                13;
                                                                  CYTOPLASMIC (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSAN-------NT 323
                                                                                                                                                                                                                                                                                                                                                                                  | | | | : : : | : | | : | | : : | : : | : : | EMKVSLQETQVSSE----FSKRDSVTNKEAVPVSKDELLEQSEVVVSTSSIQKN-KILDN 148
                                                                                                                                                                                                                                                                                                                                                                                                                       149 KKKRANFVISSPLIKEKPSNSKDASGVIDNS-------ASPLSYRKAKEVVS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243
                                                                                                                                                                                                                                                                                                                                  58 ETVNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNL 117
                                                                                                                                                                                                                                                                                                                                                                      118 EGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                ....-WNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARG5,6 protein, mitochondrial precursor [Contains: N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase); Acetylglutamate kinase (EC 2.7.2.8) (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-phosphotransferase)].
                                                                                                                                                            NISIN LEADER PEPTIDE PROCESSING SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 LRQPLKNQKVEAQPLLISNSSEKKASVYTNSHDFWDYQW------DMKY---VTNNGES
                                                                                                                                                                                                                                                                                                                                               QKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 TANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIG-NIYLSSNEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------KMGHGTEVAGQITANGNILGVAPGITVNIYRVFGEN
                                                                                                                                                                                                                                                                                              DB 1; Length 682;
                                                                                                                                                                                          MEMBRANE ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                 Indels
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D5F29313F2983EC9 CRC64;
                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                61; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                              7.7%; Score 154.5; D 21.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           857 AA
                                                                                                                                                                         PROTEASE NISP.
  an email to license@isb-sib.ch)
                                                         Interpro; IPR001899; Gram_pos_anchor.
Interpro; IPR000209; Peptidase_S8.
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                       EMBL; L11061; AAA25200.1; -.
                               X76884; CAA54210.1; -. P29600; 1GCI.
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                                                                                                                                                                                                                                                                                                                  Conservative
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679
682
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195
682
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                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 75; Conserv
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                                                   MEROPS; S08.059;
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P78586;
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HSSP;
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250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 VEAAINSGYLPILTSLAETSSGQLLNVNADVAAGELAREFEPLKIVYLNEKGGIINGNTG 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----NSITD-----VSWIYSLAGINTKYQFSFSNYG-PSTGYL
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PROSITE; PS01224; ARGC; 1.

Oxidoreductase; Transferase; Kinase; Arginine biosynthesis; NAD
Mitochondrion; Multifunctional enzyme; Transit peptide.

TRANSIT 1 1 2 MITOCHONDRION (POTENTIAL).

CHAIN 2 ACETYLGLUTAMATE KINASE.

ONATIN 2 857 N-ACETYL-GAMMA-GLUTAMXL-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.1%; Score 143; DB 1; Length 857;
23.3%; Pred. No. 0.64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REDUCTASE.
BY SIMILARITY.
AE2CEAD8FF8C4C71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD003765; AGPR_act_site; 1. PROSITE; PS01224; ARGC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000706; AGPR_act_site.
InterPro; IPR001048; Aakinase.
InterPro; IPR000534; Semialdh_dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00696; aakinase; 1.
Pfam; PF01118; Semialdhyde_dh; 1.
Pfam; PF02774; Semialdhyde_dhC; 1.
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857 #
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SEQUENCE
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                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription regulatory protein.SWII (SWI/SNF complex component SWII)
(Transcription regulatory protein ADME) (Regulatory protein GAM3).
ADME OR SWII OR GAM3 OR YPL016W OR LPA1.
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 329
                                                                        AVDEIKVA----KIVLSGLR--FGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 384
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89057455; PubMed-3143101;
O'Hara P.J., Horowitz H., Elchinger H., Young E.T.;
"The yeast ADRG gene encodes homopolymeric amino acid sequences and potential metal-binding domain.";
Nucleic Acids Res. 16:10153-10170(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             franscription regulation; Activator; DNA-binding; Nuclear protein;
284 YFPY-----KLVKAADANNVG--LOYKLNNG---NVQQVE-FATSTSANNTTANPTP
                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 65 ASN/THR-RICH.
337 385 GLN-RICH.
121 1258 C4-TYPE.
1314 AA; 147938 MW; F442D5A82013CDBD CRC64;
                                                                                                                                                                                                                                                                                                                                                        Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                              PRT; 1314 AA.
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InterPro; IPR001606; ARID.
Pfam; PF01388; ARID; 1.
SWART; SW00501; BRIGHT; 1.
                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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CHARACTERIZATION.
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P09547;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPQAI-LAKNSIID----SSNLPLQAQQQLYGG-----NNNNNSTGIANDNVI 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 NLTSNQLISN-----SDNNNNS 285
                                                                                                                                                                                                                                                                    LKMAKTNLES---AINQANTDKTT-----FDNEHPNLVEAYKALKTTLEQRATNLEGL 120
                                                                                                                                                                                                                                                                                                                                    105 TVASSTNFTSPTAVVNNAAPANVTGGKAANFIQNQSPQFNSPYDSNNSN----TNLNSL 159
                                                                                                                                                                         | | | | | : : | : : | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | | : | : | | : | | : | | : | | : | : | | : | | : | : | | : | | : | : | | : | | : | : | | : | | : | | : | : | | : | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                  NPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNATLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 NADALSNSFIKKVIQNNEQSFVGTFTNANVQP-SNYSFVAFSADVTPVNYKYARRTVWNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 TPHFITN--VQSISQNSSSSTPN--TNSNSTPNANQQFLPFNNSASN-----NG
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 79.4 kDa protein in ALD2-DDR48 intergenic region.
YMR172W OR YM8010.02.
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Length 1314;
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STRAIN-S288C / AB972;
STRAIN-S288C / C.M. Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (JUN.1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175; Indels
                                                                  Indels
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19.8%; Pred. No. 1.1;
tive 72; Mismatches
6.9%; Score 138.5; 1
20.4%; Pred. No. 1.9;
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                                                               Mismatches
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                                                               26;
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SEQUENCE 719 AA; 79415 MW;
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                                                               Conservative
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Q03213;
                                                               70;
   Query Match
Best Local S
Matches 70
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCCEAN J., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COULD BE A SPINDLE POLE BODY MOTOR. ON TRANSITION FROM
G2 TO M PHASE OF THE CELL CYCLE, THE SPINDLE POLE BODY DUPLICATES;
THE DAUGHTER POLE BODIES SEED MICROTUBLES WHICH INTERDIGITATE TO FORM A SHORT SPINDLE THAT ELONGATES TOSPAN THE NUCLEUS AT
METAPHASE. MUTATIONS AT CUT7 BLOCK SPINDLE FORMATION.
-!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
                                                                                                                                                                                                                                                                                                                                                                                                                           396 NDHASAAQKPISALSPLINSHNSTISMNYINSSIHSGVISASNSFHDLNSLNNFGTITAL 455
                                                                                                                                                                                                                                                                                                                                                                                                   -----SRILANTNSITDVSWIYS-----LAGTNTKYQF-SFSNYGPSTGY 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 LYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLS 342
                                   97 LLRISAAISAPIGTSQPTETIGEKLSNEERVNSNVSASNSTTAGTGRMLSQSLTN-DSPS 155
                                                                                                                                                           167
                                                                                                                                                                                                                                       ------DALSNSFIKKVI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE-91015362; PubMed-2145514;
Hagan I., Yanagida M.;
"Novel potential mitotic motor protein encoded by the fission yeast
                                                                                                           NEISTDQLKIFQRMDEMSARMIEMEESFNKLSNKIAEQNTWVLNLKQDNYKVMNKLNILL
                                                                                                                                                                                  216 KLVAQPSARPSTNNAQNKLAIELLNSISAVSSAYLQKMQNNGSGRQHTADLCTGDSNTHS
                                                                                                                                                                                                                                                                                 GINOHRTTNGTIDVNTNTAQLNNQFSNALNTILPDQQHNRNNVSQNINQSLPNRQLGPVI
                                                                                                                                                                                                                                                                                                                                                         336 NIQANQNQSQVLIHNTNIHQQVNRSPISFPNASIDKPFKLNPNGIKRRRRNTQSNNNASI
                                                                                                                                                           ---NQIRNNL-VDLYNKASSLITKTLDPL--NGGTLLDSNEITTANKN---
                                                                                                                                                                                                                                                                                                                      ----QNNEQSFV-GTFTNANVQPSNYSFVAFSAD----VTPVNYKYARRTVWNGDEPS-
-----SLSSAYSEAETVNNNLNA------TLEQLKMAKTNLESAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 GLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKIPGYRRPGT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 SLPSLALDNASFPPNONVIPPIINNTOOPLSFSQLINQDSTTS-----
                                                                              NQANTDK - - - - TTFDNEHPNLV - - - EAYKALKTTLEQRATNLEGLSSTAY -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota: Schizosaccharomycetes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Inssin-11ke protein cut7.
CUT7 OR SPAC25G10.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                           -----INNTLSTINEOKTNA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 347:563-566(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
      -LQDYAKIEA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUT7_SCHPO
P24339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVNLEVQTLDRLLQKVKEHSEDNTKEKHQQL---LDLLESLVGNNDNLIDSIKTPHTELQ 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 QVE----FATSTSANNTT------ 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEQLKMAKTNLESAINQANTDKTTFDNEHPN-----LVEAYKALKTT----LEQRATNLEG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            623 NGYFTLLNDFNASMEELLNTHSNQLLISMTKITEHFQSLDEALQSARSSCAVPNSSLDLI 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            683 VSELKDSKNSLLDALEHSLQDISMSSQKLGNGISSELIELQKDMKESYRQLVQELRSLYN 742
                                                                                                                                           PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Cell division; Microtubules; ATP-binding; Coiled coil; Mitosis; Cell cycle; Phosphorylation; Repeat..
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 NGQ-TQLEAARMELTDLINAKA-MTLASL----QDYAKIEASLSSAYSEAETVNNKNAT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKNINNTLSTINEQ-KTNADAL----SNSFIKK---VIQNNEQSFVGTFTNANVQPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 YSFVAFSADVTPVNYKYARRTVWNG----DEPSSRILANTNSITDVSWIYSLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTNTKYQ-------QYKLNNGNVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1085;
                                                                                                                                                                                                                                                                                                                                  Ŷ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 LSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEIT------
                                                                                                                                                                                   Phosphorylation; Repeat.
StingsIN-MOTOR (BY SIMILARITY).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                   SIMILARITY)
SASNPRKREPPPTIDTGYPDRSDTNSPT
LRAILGNDVSLLLLTL (IN REF. 1)
MW, 5669277875559D58 CRC64;
                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY CDC2) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | | : : | ||| : | :| 1023 WTRDSSLIKETTULNLDSDKKFVRETYTSSNQTNEPDV--YDKP 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352. ---- ELSVPTGEGNMNKVAPMIGNIYLSSNENNADKIPGYRRP 390
                                                                                                                                                                                                                                              COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 135.5; DB 1;
20.9%; Pred. No. 2.2;
live 76; Mismatches 182;
                                                                                                                                                                                                                                                           ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein MG338 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1271
send an email to license@isb-sib.ch)
                                                                                                                PRINTS; PR00380; KINESINHEAVY
                                                                                  InterPro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
                         EMBL; X57513; CAA40738.1; -. EMBL; Z70691; CAA94636.1; -. PIR; S14032; S14032.
                                                                                                                                                                                                                                                                                                                                                              1085 AA; 122133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                     97; Conservative
                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                               SM00129; KISC;
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                       HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y338_MYCGE
P47580;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                              NP_BIND
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
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Y338_MYCGE
                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                      DOMAIN
                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                           REPEAT
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252 SIT--DVSWIYSLAGINTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S15330; FCSOAG.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003599; Ig.
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00746; Gram_pos_anchor; 1.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION OF IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Microbiol. 5:843-849(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1164 AA; 131051 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X59771; CAA42442.1; -.
                                                                            584 DVCDLAKKLLKNNTNLSET 602
                                                                                                                                                                                                                                                  Streptococcus agalactiae.
                                                     310 QOVEFATSTSANNTTANPT
                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell wall; Transmembra
Immunoglobulin domain
                                                                                                                                                                                                                                                                            Streptococcus.
NCBI_TaxID=1311;
                                                                                                                                                                                                                                                                                                                                                                                                   binding regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1141
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439
827
1131
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P27951:
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                    Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchmann J.L., Weidmann J.F., Small K.V., Sandusky M., Fuhrmann J.L., Tomb J.-F., Dougherty B.A., Saudek D.M., Phillips C.A., Marrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANK--NINNTLSTIN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTSSNL-----NPLDKFIKSSSATTVMK----SAMTKSQEVTSDNNGFNVKSEFLKIN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E--OKTNADALSN--SFIKKVIQNNEQSFVGTFTNANVQPSNYS------FVAFSAD 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : | : | : | | : | | TT---QKQQQKPVYVRGDDAIYAFHIDGGNYFLENSSPNKRNFEKQAEVLLMRFLQGQTN 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 TLE-----QLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSLSSSGSDNSSNTQSFWKQVQALNNSSQTATIFDAVRMESNSSQAQVVTSNLLVSLSSK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 VTPVNYKYARRTVW-NGDE----ILANTN 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                  sequencing.";
J. Bacteriol. 175:7918-7930(1993).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 KDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAK-IEASLSSAYSEAETVNNNLNA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 LLDFENKYSASKVLISKNNILSVLKTVNLSAAVIDQYH-YLLNNKTELTTTTTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98;
                                                                                                                                                                                                                                                                                       Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III; "A survey of the Mycoplasma genitalium genome by using random
                          Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL LIPOPROTEIN MG338.
N-ACYL DIGLYCERIDE (POTENTIAL).
W; FCE6042067310A70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.6%; Score 132; DB 1; Length 1271; 22.2%; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                           (Potential).
-!- SIMILARITY: BELONGS TO THE MG307 / MG309 / MG338 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
4ypothetical protein; Lipoprotein; Membrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                             STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; PubMed-7569993;
                                                                                                                                                                                                                                                         STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; PubMed-8253680;
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                                                                                                                                                                                                                                                 SEQUENCE OF 1023-1114 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U39715; AAC71563.1; -.
                                       Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U01809; AAD12341.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
1271
27
               4ycoplasma genitalium.
                            Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                SEQUENCE FROM N.A.
                                                       NCBI_TaxID-2097;
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                                                                                                                                                                                                                                                                                                                     sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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EXTRACELLUIAR (POTENTIAL).

EXTRACELLUIAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

IG-LIKE DOMAIN.

IGA-BINDING (POTENTIAL).

IGA-BINDING (POTENTIAL).

PRO-RICH REPEATS.

CONSERVED IN GRAM-POSITIVE COCCI SURFACE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91312121; PubMed-1857207; Jerlskroem P.G., Chhatwal G.S., Tlumis K.N.; Jerlskroem P.G., chhatwal G.S., Tlumis K.N.; The IgA-binding beta antigen of the c protein complex of Group B streptococci: sequence determination of its gene and detection of two
533 NFSKDNVSFSVDLFGSNSEFR-SWANRN-TTLKLYTALTIMLENGTSN-----NNGQK 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65DE94AF720A5474 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [gA FC receptor precursor (Beta antigen) (B antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Receptor; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                     1164 AA
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Gaps

Indels 122;

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89;
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                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SADVIPVNYKYARRIVWNGDEPSSRILANTNSITDVSWIYSLAGINTKYQFSFS----N 275
                                                                                                                                                                                                                                                                                                                                                                          488 YKTNTDNHKIAEITIKNLKLNESQTVTLKAKDDSGNVVEKTFTITVQKKEEKQVPKTPEQ 547
                                                                                                                                                                                                                                                             396 HSKLKQVVEDFRKKFKTSEQVTPKKRVKRDLAANENNQOKI-----ELTVSPENI---- 445
                                                                                                                                                                                                                                                                                                           446 ------TVYEGEDVKFTYTAKSDSKTTLDFSDLL----TKYNPSVSDRISTN 487
                                                                                                                                                                                                                                                                                                                                                 276 YGPSTG---YLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANP-TPAV 331
                                                                                                                                                                         TLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNI 168
                                                                             LONLAQKSLEELDKATTN----EQATQVKNQFLENAQKLKEIQPLIKETNVKLYKAMSE 344
                                  Gaps
                                                           7 KKDANPNNGQTQLEA-ARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AET
                                                                                                                                                                                                  SLEQVEKELKHNSEA-----NLEDLVAKSKEIVREYEGKLNOSKNLP--ELKQLEBEA
                                                                                                                                                                                                                                   NNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVAF
                                77;
    Length 1164;
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Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID-31273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.; "A reticulocyte-binding protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1251 AA; 143741 MW; 54BA51C7404AC572 CRC64;
                                  Indels
                                                                                                                      60 VNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL----
     6.6%; Score 131.5; DB 1; 22.8%; Pred. No. 4;
                                  51; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Reticulocyte binding protein 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1251 AA
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MEDLINE-92315338; Pubmed=1617731;
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                                     84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             332 DEIKVAKIV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                         548 KDSKTEEKV 556
          Query Match
Best Local Similarity
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Q00799;
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SEQUENCE
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RBP2_PLAVB
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Query Match Best Local Similarity

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PSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANN-----TTA-- 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 VGIKITPELALFELLGDAKLKTAQELKFESKNNVVLETENMSKNTNELDVHKNIQDAYKV 791
                                                                                                                                                                                                                                                                                                                                                                                                       518 SKGNYEIGFLEKLEEIGKNRKLKVDITKKS---INSTVG--NFSSLFNNFDLNQYDFNKN 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 INNTLSTINEQKTNADALSNSF---IKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 TPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIY----SLAGTN---TKYQFSFSNYG 277
                                                                                                                                                                                                 LEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQ 127
                                                                                                                                                                                                                                                                           517
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                                                          QTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAE-----TVNNNLNAT 67
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                                                                                                                                                                                                                                                     614 LRLEAQKEKVNLLNKEEEANKYLRDVKKVESFRFIFNMKESLDKINEMIKKEQLTVNEGH
                                                                                                      "Molecular analysis of three major wall-associated proteins of
Bacillus subtilis 168: evidence for processing of the product of
gene encoding a 258 kDa precursor two-domain ligand-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=168 / BGSC1A1;
MEDLINE=97124196; PubMed=8969509;
Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai Miwa Y., Fujita Y.;
"Sequencing of a 65 kb region of the Bacillus subtilis genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
70; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 30, Created)
(Rel. 30, Last sequence update)
(Rel. 41, Last annotation update)
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STRAIN=168 / BGSC1A1;
MEDLINE=95219088; Pubmed=7704263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
       Conservative
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SEQUENCE FROM N.A.
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Q07833;
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Length 2334;

DB 1;

6.4%; Score 128.5; bred, No. 14;

Query Match

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         covering the gnt-sacxY region.";
Microbiology 142:31123(1996).
-!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
-!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
MOTILITY, SECRETION OR DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED
INTO THE MEDIUM.
-!- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE
                                                                                                                     SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
                                                                                                                                                                                                                                                                                                                                                                                                                   1-3.
31 x 21 AA APPROXIMATE TANDEM REPEATS OF
44)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
2-1.
                                                                                                                                                                                                                                                                                                                                                Repeat. Signal, Complete proteome.
1 28 OR 32 (POTENTIAL)
29 2334 WALL-ASSOCIATED PROTEIN.
504 869 3 X 101 AA APPROXIMATE TANDEM REPEATS.
                                                                                    101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED MOTIF REPEATED 31 TIMES.
containing the lic and cel loci, and creation of a 177 kb contig
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2-11.
2-11.
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22-6.
2-8.
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EMBL; D31856; BAA06556.1; -.
EMBL; D29985; BAA06260.1; -.
EMBL; D83026; BAA11683.1; -.
EMBL; 299124; CAB15959.1; -.
PIR; S32920; S32920.
Subtilist; BG10797; wapA.
InterPro; IPR003305; CBD_6.
Pfam; PF02018; CBD_6: 1.
Cell wall; Repeat; Signal; Comp
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Gartison K., Mackrell A.J., Fessler J.H.;
Gartison K., Mackrell A.J., Fessler J.H.;
Gartison K., Mackrell A.J., Fessler J.H.;

"Drosophila laminin A chain sequence, interspecies comparison, and domain structure of a major carboxyl portion.";
J. Biol. Chem. 266:22899-22904(1991).

-i- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
                                                                                                         1772 SVVNKEQNTTKKRTFDNKNRLTELTDRGGSQTWTYPSDSDKLK---TFSWIHGDQKGTNQ 1828
                                                                                                                                                                                                                                                                    1944 GNRKTVTTIKDGSSKTVNASFNIMNQLTKVNDESISYD------KNGNRTSDGKF 1992
                                                                                                                                                                                               1829 FTYNKLDOMIEMKDSTSSYSFDYDENGNVOTFIT-GNGGGTSFSYDERNLVSSLHIGDKN 1887
                                                                                                                                                                                                                                                                                                                               202
                                                                                                                                                                                                                                           -----EAYK----ALKTTLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPL 150
                                                                                                                                                                                                                                                                                                                                                                                                                    206 TNANVQPSNYSFVAFSADVTP-VNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 TNTKYQFSFSN-----YGPS-----TGYLYFPYKLVKAADANNVGLQYKLN-NGN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                      Gaps
                                                               61
                                                                                                                                                                                                                                                                                                                               151 NG----GTLLD-SNEITTANKNINNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1993 TYTWDAEDNLTAVTKKGEDKPFATYKY------DEKGNRIQKTVNGKV-TNYFYDGDS
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                                                               4 SITKKDANPNNGQTQLEAARM-ELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henchcliffe C., Garcia-Alonso L., Tang J., Goodman C.S.; "Genetic analysis of laminin A reveals diverse functions during morphogenesis in Drosophila."; pevelopment 118:325-337(1993.")
                      113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2088 I----IAISDSTGKTVAKYQYDAWGNPTKTEASDEVKDNRYRYAGYQYDEET 2135
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                                                                                                                                                      ---NNLNATLEQLKMAKT------NLESAINQANTDKTTFDNEHPNLV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 VQQVEFATSTSANNTTA-----NP--TPAVDEIKVAKIVLSGLRFGQNT 350
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Kusche-Gullberg M., Garrison K., Mackrell A.J., Fessler L.I.,
                      Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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22.1%; Pred. No. 14; ive 56; Mismatches
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MEDLINE-94038678; PubMed-8223265;
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LANA OR LAMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic sequence.";
EMBO J. 11:4519-4527(1992).
                    Conservative
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Best Local Similarity
Matches 91; Conserv
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LAMININ EGF-LIKE 10.
LAMININ EGF-LIKE 11 (INCOMPLETE).
DOMAIN IV'
LAMININ EGF-LIKE 13.
LAMININ EGF-LIKE 13.
LAMININ EGF-LIKE 13.
LAMININ EGF-LIKE 14.
LAMININ EGF-LIKE 16.
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LAMININ G-LIKE 2.
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LAMININ G-LIKE 4.
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LAMININ G-LIKE 10.
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CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
COMPLETE LOSS-OF-FUNCTION DIVERSE FUNCTION BURENG MORPHOGENESIS IN DROSOPHILA.
COMPLETE LOSS-OF-FUNCTION MUTATIONS LEAD TO LATE EMBRYONIC
LETHALITY. CERTAIN PARTIAL LOSS-OF-FUNCTION MUTATIONS GIVE RAISE
TO ESCAPER ADULTS, WHICH HAVE ROUGH EYES ASSOCIATED WITH CHANGES
IN CELL FATE AND PATTERN, MISSHAPPEN LEGS AND DEFECTS IN WING
STRUCTURE.
DIFFERENT POLYPETIDE CHAIRS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISJULFIDE CHAIRS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISJULFIDE CHAIRS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISJULFIDE CHAIRS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISJULFIDE CHAIRS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISJULFIDE CHAIRS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISJULFIDE CHAIRS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISJULFIDE CHAIRS STRUCHURE
COMPRESSED IN HEMOCYTES, WHICH ALSO STWINESIZE COLLAGEN IV.

TISSUE SPECIFICITY: NURLY FORMED MESODERM AND LATER PROMINENTLY
EXPRESSED IN HEMOCYTES, WHICH ALSO STWINESIZE COLLAGEN IV.

THOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COLLED COIL STRUCTURE.

TO DOMAIN: THE ALPHA-HELICAL DOMAINS IN COMAIN VI).

TO SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV (DOMAIN VI).

SIMILAR TO LAMININ DOMAIN IV).

SIMILAR TO LAMININ S LAMININ G-LIKE DOMAINS.
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LAMININ N-TERMINAL (DOMAIN VI).
LAMININ BGF-LIKE 1.
LAMININ BGF-LIKE 3.
LAMININ BGF-LIKE 3.
LAMININ BGF-LIKE 4.
LAMININ EGF-LIKE 5.
LAMININ EGF-LIKE 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00023; EGF_1; 17.
PROSITE; PS0126; EGF_1; 17.
PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
PROSITE; PS0025; LAM_G_DOMAIN; 5.
Glycoprotein; Basement membrane; Extracellular matrix; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
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EMBL; L07288; AAA28662.1; --
EMBL; M75882; AAA28661.1; --
HSSP; P02468; TLE.
Flybase; FB90002526; LanA.
InterPro; IPR000561; EGF-like.
InterPro; IPR001886; LanMI.
InterPro; IPR001984; Laninin_B:
InterPro; IPR001791; Laninin_B:
InterPro; IPR001791; Laninin_B:
InterPro; IPR001791; Laninin_B:
Ffam; PF00052; laminin_B: 1.
Pfam; PF00054; laminin_B: 1.
Pfam; PF00055; laminin_B: 1.
ProDom; PD002082; LamNI; 1.
ProDom; PD002082; LamNI; 1.
ProDom; PD002081; LamNI; 1.
SWART; SW00109; EGF_LAM; 1.
SWART; SW00101; EGF_LIKe; 1.
SWART; SW00136; LamM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 LNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSST 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNAD 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 GSQSVSS----ASGSSSSFPQST----SSASTASGSATSNSLSSITSSASSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 ALSNSFIKK-----VIQNNEQSF---VG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 VYGDLLVKKSKETYPGTEFDISGENFDVTGN--FNAEESAATSASIYSFTPSSFDNSGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : | | | | : | | | : | SLSLSKSKKGEVTFSPYSNSGAFSF----SNAI-----INGGSVSGLQRRDDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYL---
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                                                                                                                                                                                                                                                  POTENTIAL.
HYPOTHETICAL PROTEIN ..... (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
"-1.INKED (GLCNAC. .) (POTENTIAL).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                    73; Conservative 100; Mismatches 152; Indels 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 106.1 kDa protein in GLX1-GDA1 intergenic region.
YEL043W OR SYGP-ORF14.
                                                                                                                                                                                                                                                                                                                                                                                                   Length 995;
   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                  SGD; SO001431; YIL169C.
InterPro; IPR0040099; Chemotaxis_transducer.
InterPro; IPR0040727; T_SNARE.
Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497 DIFIGOTVVFKGEGVLAVDPTETNATPIPVVGY 529
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 128;
Pred. No. 5
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Best Local Similarity 16.1%;
                                                                                                                                                                  EMBL; Z46921; CAA87023.1; -.
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99735 N
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695 AA;
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P32618;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2746 GNGP-----ERITSDKYVADGRWYQAVVDRMGPNAKLTIREELPNGD-----VVEHS 2792
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2502 TDLLQRARQSLQKVQD--DLEPRLNASAGKVQKISAVNNATEHQLK----DINKLIDQLP 2555
                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIR-----NNLVDLYNKA 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 ANNTTANPTPAVDEIKVAKIVLSGL-----RFGQN---TIELSVPTGEGNMNKVAPMI 369
                                                                                                                                                                                                                                                                                                                                                                    27 TDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNATLEQLKMAKTNLESAINQ-- 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-S288C / AB972;
STRAIN-S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser I
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones I
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                      DB 1; Length 3712;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 99.7 kDa protein in SDL1 5'region precursor.
                                                                                                                                                                                                                                                                                                                                     155;
                                              SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
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48; Mismatches
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SIMILARITY.
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Pred. No. 24;
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   6.48;
                                                                                                                                                                                                                                                                                                                  Best Local Similarity 23.4 Matches 91; Conservative
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                                              1447
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YIQ9_YEAST
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NCBI_TaxID=4932;
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GPI-ANCHOR
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Q12355;
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PST1_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETVNNNLN-ATLE------QLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 ITKKDANPNNGQTQLEBARMELTDL----INA-KAMTLASLQDYAKIEASLSSAYSEA 57
                                                                                      STRAIN-S288C / AB972;

STRAIN-S288C / AB972;

Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Cherry J.M. Chury B., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Obefrer P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wel Y., Yelcon M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTL-DPL--NGGTLLDSNEITTA
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                                                                                                                                                                                                          FIBRONECTIN TYPE III DOMAIN.
MEDLINE-97148176; Pubmed-8994808;
Bateman A., Chothia C.;
"Fibronectin type III domains in yeast detected by a hidden Markov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.3%; Score 127; DB 1; Length 956;
19.7%; Pred. No. 5.5;
tive 86; Mismatches 163; Indels 176;
                                    :
                                                                                                                                                                                                                                                             Curr. Biol. 6:1544-1546(1996).
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKN------DINTLSTINEQKTNADAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIBRONECTIN TYPE-III.
                                   Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., I
Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 956 AA; 106132 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              SGD; SG000769; YEL043W.
InterPro: IPR003961; FN_III.
Pfam; PF00041; fn3; 1.
SMARY; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U18779; AAB64999.1;
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Best Local Similarity
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                              SECUENCE FROM N.A.
        NCBI_TaxID=4932;
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MEDLINE-20469049; PubMed-11016834;
Terashima H., Yabuki N., Arisawa M., Hamada K., Kitada K.;
Terashima H., Yabuki N., Arisawa M., Hamada K., Kitada K.;
Terashima H., Yabuki N., Arisawa M., Hamada K., Kitada K.;
Tersponse encoding glycosylphosphatidylinositol

"Up-regulation of genes encoding glycosylphosphatidylinositol

"GPI)-attached proteins in response to cell wall damage caused by
disruption of FKB1 in Saccharomyces cerevisiae.";
Mol. Genet. 264:64-74(2000).

"SURELIULIAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR AND
SECRETED BY REGENERATING PROTOPLASTS.

"SURLEAULIAR TY: BELONGS TO THE SPS2 FAMILY.
                                                                                                                                                                                                                                          730 QTSNATNIPWHPQSLLAATLNDPSLQSFVRSGSFYSAPQPANSLQNNINGNETENISPR 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=96381250; PubMed-8789263;
MEDIINE=96381250; PubMed-8789263;
Brandt P., Ramlow S., Otto B., Bloecker H.;
"Nucleotide sequence analysis of a 32,500 bp region of the right arm
of Saccharomyces cerevisiae chromosome IV.";
---PSTGYLXFPYKLVKAADANNVGLQYKLNNGNVQ 310
                                                                               678 KGFTIDELDNYWIKQQPQVRSINESLFSTIGIPMSSYK-----ANPVISPY--SSSHLR 729
                                                                                                                                                              354
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Pardo M., Monteoliva L., Pla J., Sanchez M., Gil C., Nombela C.;
"Two-dimensional analysis of proteins secreted by Saccharomyces cerevisiae regenerating protoplasts: a novel approach to study the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C / AB972;
Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                    790 ISSDEWLLVPWLSPRLSNDVPIVPGWNTTLTPSHSWILTMWHQPTADWI 838
                                                                                                                                                                                                                                                                                                                             ------VPTGEGNMNKVAPMIGNIYLSSNENNADKI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                           311 QVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protoplast secreted protein 1 precursor.
PST1 OR YDR055W OR D4214 OR YD9609.09.
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EMBL; Z74351; CAA98873.1; --
EMBL; Z49209; CAA89084.1; --
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COMPLUYEAST-2DPAGE; Q12355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keast 15:459-472(1999).
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                                                                                                            PTM: MEROZÓITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 VGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEK-----KKLYQAQYDLSI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 FDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 YNKQ---LEEAHN-LISVLEKRIDTLKK-----NENIKELLDKINEI--KNPPPAN 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LASLQDYAK-----IEASLSSAYSEAETVNNNLNATLEQLKMAKTNLESAINQANTDKTT 91
                                                      Pan W., Tolle R., Bujard H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 KVIQNNEQSFVGTFTNANVQPSNYSFV-----AFSADVTPVNYKYARRTVWNGDEPS
 Plasmodium falciparum merozoites: studies at the genetic level.";
EMBO J. 4:3823-3829(1985).
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                                                                                                                                                                                                                                                                                 EMBL, X03371; CAA27070.1; -.
PIR: A25120; SAZOK1.
Interpro: IPR000561; EGF-like.
Pfam: PF00008; EGF: 1.
Malaria, Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1630;
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MEMBRANE ANCHOR.
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Matches 86
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TSFAADSLESITDSLNLQSLTILT-----SASFGSLQSVDSIKLITLPAISSFT 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 SVKLSSTSKSOSS-----QTTAKVSKSSSKAEEKKFTSGDIKAAASASSVSSSGASS-- 410
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                                                                                                                                                                                                                                                                                                                             Indels 105; Gaps
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01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-86136024; PubMed-3004972; Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U., Stunnenberg H., Bujard H.; "Pelymorphism of the precursor for the major surface antigens of
ID PROTEIN 1. FORM (POTENTIAL).
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NCBL_TaxID-5839;
                                                                                                                                                                                                                                                         CRC64;
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Matches 73; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGUENCE FROM N.A. MEDILIBE 48601435; PubMed-2995820; MEDILIBE 86014355; PubMed-2995820; Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11- PTM: MEROZÓTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holder A.A.;
Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                   13-AUG-1987 (Rel. 05, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
(PMMSA) (P195).
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Interpro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites."; Nature 317:270-273(1985).
328 TPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADK
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Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium
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AA; 187618 M
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Gaps

Indels 113;

6.3%; Score 126.5; DB 1; 20.7%; Pred. No. 11; vative 62; Mismatches 155;

Conservative

86;

Similarity

Query Match Best Local S: Matches 86

Length 1639;

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192 KVIQNNEQSFVGTFTNANVQPSNYSFV-----AFSADVTPVNYKYARRTVWNGDEPS 243
                                                                                                                                                                                                                                                                    -----TNSITDVSWIYSLAGINTKYQFS 272
                                                                                                                                                                                                                                                                                                                                                           441 KNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKL-LNEIYDSK 499
                                                                                                                                                                                                                                                                                                                                                                                                   273 FSNYGPSTGY----LYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANP 327
                                                                                                        33 YGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEK-----KKLYQAQYDLSI 287
                                                                             92 FDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLN 151
                                                                                                                                                              ---SNSFIK 191
37 LASLQDYAK----IEASLSSAYSEAETVNNNLNATLEQLKMAKTNLESAINQANTDKTT 91
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Q48674 Indecodedum
Q48674 Indecodedum
Q49545 mycoplasma
Q96764 Indecodedum
Q96764 Indepasma
Q9908 ureaplasma
Q9908 ureaplasma
Q91019 staphylococ
Q91615 staphylococ
Q91615 staphylococ
Q91612 taphylococ
Q91612 taphylococ
Q91612 propplasma
Q49548 mycoplasma
Q49546 mycoplasma
Q49546 mycoplasma
Q49546 mycoplasma
Q49546 mycoplasma
Q956109 plasmodium
Q91199 mycoplasma
Q95889 helicobacte
Q96748 salmonella
Q96748 schizosacch
                                       Q99u54 staphylococ
Q931r6 staphylococ
Q49547 mycoplasma
                                                                                               099qr6 staphylococ
099u53 staphylococ
097te6 clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2096;
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29817 MW; 8B25DE0CD5C85CA2 CRC64;
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Last annotation update)
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larity 97.1%; Pred. No. 2.2e-51;
Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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                                     Q99U54
Q931R6
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
TM-1 (FRAGMENT).
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NON_TER 271
SEQUENCE 271 AA; 29817
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RESULT
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                                                                                                                                  June 12, 2002, 10:50:40; Search time 48.58 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Minimum DB s Maximum DB s

Database

Searched:

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Gaps 61

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STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 181

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Result ş Created)

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01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, PMGA1.4 PROTEIN PRECURSOR.
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Matches 173; Conserv
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 ENNVALQYTLNSGSAQEVNFAPTVKTSVSADSSGDSNNQTESAAETMPVTSDLNPAPTVS 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | SDNGRTSLISSTSDNSSTLTEVSWIYSLSGAGTKYSLTENYYGPSTGYLYFPYKLVKEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 TAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 GDEPSSRILA----NTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAAD
                                                                    Pherr G.T., Branton S.L., Hanson L.A., Minion F.C., Lott B.D., May J.D., Hughlett M.B.;
"A novel pMGA-like gene from the F-strain (vaccine strain) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 DINIAKLTLSNLKFGSNTIEFSVPTEPS--NKVAPMIGNMYLTSNIANEAKV 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
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43.4%; Pred. No. 2.5e-33;
Live 75; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma gallisepticum.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF120770; AF729524.1;
SEQUENCE 671 AA; 71898 M; 4D6AE6BS9175D679 CRC64;
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Last annotation update)
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Best Local Similarity 43.4%
Matches 179; Conservative
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| PSSRI 271
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Q9L8D6;
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STRAIN=S6;
MEDLINE=95010739; PubMed=7925999;
Markham P.F., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D.,
Browning G.F., Whithear K.G., Walker I.D.;
"The organisation of the multigene family which encodes the major cell
surface protein, pMGA, of Mycoplasma gallisepticum.";
FEBS Lett. 352:347-352(1994).
EMBL: L28424; AAA62418.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 NLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 AADANNVGLQYKLNNGNVQQVEFATS-----TSANN-----TTANPTPAVD 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 DANPING-----QTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTP-----VNYKYARRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 WNGD-----EPSSRILANTNSITDVSWIYSLAGINTKYQFSFSNYGPSTGYLYFPYKLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 EIKVAKIVLSGLRFGQNTIELSVP-TGEGNMNKVAPMIGNIYLSSNENNADK 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma imitans.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 702;
                                                                       Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                           25 POTENTIAL.
75517 MW; B70AC874FE85055C CRC64;
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42.0%; Pred. No. 4.8e-33;
tive 84; Mismatches 116;
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NCBI_TaxID=29560;
                                                                                                         Mycoplasmataceae; Mycoplasma
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SEQUENCE FROM N.A.
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STRAIN-4229

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PRT;

PRELIMINARY;

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67 ILEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYN 126
                                                                                                                                                                                                                                          62 NNLNATLEOLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEORATNLEGLS 121
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                                                          11 NPNNGQT----QLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNA
                                                                                                                                                                      127 QIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNADALS
                                                                                                                                                                                      187 NSFIKKVIQNNEQSFVGTFTNAN--VQPSNYSFVAFSADVTP------VNYKYARRT
                                                                                                                                                                                                                                                                                236 VWNGD---EPSSRILANTNSITDVSWIYSLAGINTKYQFSFSNYGPSTGYLYFPYKLVKA
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STRAIN-HS;
STRAIN-HS;
Shen O.C., Bi D.R., Weng C.J.;
Sequence analysis of the pMGA multigene family of Mycoplasma gallisepticum strain HS ":
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF275312; AF91414.1; -
SEQUENCE 680 AA; 72909 MW; AZABCG500E3DFE47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2096;
  Length 584;
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  40.2%; Score 805; DB 2; Length 58
42.4%; Pred. No. 7.6e-32;
Live 72; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                         ADANNVGLQYKLNNGNVQQVEF------ATST----
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01-0CT-2000 (TrEMBLRE1. 15,
01-0CT-2000 (TREMBLRE1. 15,
01-0CT-2000 (TREMBLRE1. 15,
ADHESIN PMGA1.3.
Query Match
Best Local Similarity 42.49
Matches 180; Conservative
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Best Local Similarity 39.84
Matches 164; Conservative
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                                                                                                                                                                                                                                                                                             59 TVNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLE 118
                                                                                                                                                                                                                                                                                                                       94 TTANNANATLKDVNDAKAALQTAISDAANAKTEFDKANLGLVSAYAKLKETLKSETTNLD 153
                                                                                                                                                                                                                                                                                                                                                     GLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                       KDANPNNGQT-----QLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAE 58
                                                                                                                                                                                                                                                      KTNADALSNSFIKKVIQNNEQSFVGTFTN----ANVQPSNYSFVAFSADVTP-----
                                                                                                                                                                                                                                                                                                                                                                                                                           --VNYKYARRIVWNGDEPS---SRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTG
MEDLINE-99392472; PubMed-10463176;
Markham P.F., Duffy M.F., Glew M.D., Browning G.F.;
"A gene family in Mycoplasma imitans closely related to the pMGA family of Mycoplasma gallisepticum.";
Microbiology 145:2095-2103(1999).
EMBL; AF141940; AAD39483.1;
                                                                                                                                                                                                              36;
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"Sequence analysis of the pMGA multigene family of Mycoplasma gallisepticum strain HS.";
Submitted (JUN.2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275312; AAF91415.1;
InterPro; IPR001986; EPSP_Syntase.
FROSITE; PS00104; EPSP_SYNTHASE_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma gallisepticum.
Bacteria; Firm.cutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2096;
                                                                                                                                                                                ; Score 826; DB 2; Length 632;
; Pred. No. 8e-33;
65; Mismatches 120; Indels
                                                                                                                          VLHA1.
173F5B12E705BE47 CRC64;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                POTENTIAL.
                                                                                                                                       66959 MW;
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Best Local Similarity 45.3%
Matches 183; Conservative
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18
632 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QIRNNLVDLYNKASSLITKTLDPLNG--GTLLDSNEITTANKNINNTLS--TINEQKTNA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289
                                                    290 VKAADANNVGLQYKLNNGNVQQVEF--------ATSTSANNTTANPTPAV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 GIKNHLSKLFDTGSAITAKTLDPTSGERPTLEKVNE---ANNGIKMAISPESLKKWKGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTP-----VNYKYARRTVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 NPNNGQT----QLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNA
                                                                               TVWNGD-----EPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKL
                                                                                                                                             354 VKTSD--KVGLQYKLNQADPVAIQFSEAAATASAPAETDGRQESAETATANEKVNPMPSV
                   QEKYSAILSEINAASSTAEEIVKQTLNPVNG-----NLPVVAALNAENTKILEAIKEEK
                                         INEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARR
                                                                                                                                                                                                                                                                                                                                                                                    MEDILIER-95010739; PubMed-7925999;
Markham P.F., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D.,
Browning G.F., Whithear K.G., Walker I.D.;
"The organisation for he multigene family which encodes the majo
surface protein, poof, of Mycoplasma gallisepticum.";
FEBS Lett. 352:347-352(1994).
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                                                                                                                                                                                                                                                                                                                Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                  332 DEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADK 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 702;
                                                                                                                                                                              STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--
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75537 MW; 273E8915FEE57B9F CRC64;
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Last annotation update)
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41.6%; Pred. No. 2.8e-29;
cive 62; Mismatches 127;
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NCBI_TaxID=2096;
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01-DEC-2001
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                                                                                       NTTANPIPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNA 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 AAQYAGIKMHLSGLYDAGKAITTKTLEPVEGDP-LTADVVMMANTKIVEAIKDEVLNPQK
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                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
STRAIN=PG31, ATCC19610;
MEDILE=99003182; PubMed=9784576;
MIDLIN FAYDO D.M., van Santen V.L., Dybvig K., Panangala V.S.
A protein (M9) associated with monoclonal antibody-mediated agglutination of Mycoplasma gallisepticium is a member of the I
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42.3%; Pred. No. 6.2e-29;
iive 64; Mismatches 123; Indels
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EMBL, AF032890; AAC69269.1; -.
SEQUENCE 645 AA; 69876 MW; 5A2F29572CFAE055 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Matches 172; Conservative
ANNVGLQYKLNNGNVQQVEF
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                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                          63
                           Markham P.F., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D., Browning G.F., Whithear K.G., Walker I.D.; Pre organisation of the multigene family which encodes the major surface protein, PMGA, of Mycoplasma gallisepticum."; FEBS Lett. 352:347-352(1994).
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                                                                                                                                                                                                                                                                                                                                          NPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQKTN
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NCBI_TaxID=2096;
                                                                                                                                                                                                                                                                                 Length 650;
                                                                                                                                                                                                                                                                              37.1%; Score 744; DB 2; Length 65
42.9%; Pred. No. 7.9e-29;
ive 62; Mismatches 127; Indels
                                                                                                                                STRAIN=S6;
Markham P.F.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: U90714. ABB50152.1;
                                                                                                                                                                                                                         HAEMAGGLUTININ.
3ABACDB65940EBBB CRC64;
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Last annotation update)
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 STRAIN=S6;
MEDLINE-95010739; PubMed-7925999;
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650 HA
70249 MW;
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Best Local Similarity 42.9%
Matches 172; Conservative
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26
650 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DANPINGO-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-PG31, ATCC19610;
MEDLINE-99003182; PubMed-9784576;
Liu L., Payne D.M., van Santen V.L., Dybvig K., Panangala V.S.;
A protein (M9) associated with monoclonal antibody-mediated agglutination of Mycoplasma gallisepticum is a member of the pMGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNADALSNSF1KKV1QNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 ARRIVW-NGDEPSSRILANT----NSITDVSWIYSLAGINTKYQFSFSNYGPSTGY
                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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                                                                                                                                                                                                                                                                                                                                                                   37.2%; Score 745; DB 2; Length 644;
42.3%; Pred. No. 7e-29;
ive 65; Mismatches 122; Indels
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                                                                                                                                                                                                                                                                                                                         644 AA; 69866 MW; 8B9F352B13FBDE5C CRC64;
                                         Last sequence update)
Last annotation update)
               644 AA
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EMBL; AF053978; AAC69274.1; -.
Hypothetical protein.
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049495; 008060;
01-NOV-1996 (TYEMBLYEL). 01, C3
01-NOV-1998 (TYEMBLYEL). 01, L6
01-NOV-1998 (TYEMBLYEL). 08, L6
HAEMAGGLUTININ PRECURSOR.
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NCBI_TaxID=2096;
                                                                                                                                Mycoplasmataceae; Mycoplasma
                                                                                                     Mycoplasma gallisepticum.
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Best Local Similarity 42.3%
Matches 172; Conservative
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             PRELIMINARY;
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Best Local Similarity 41.0
Matches 166; Conservative
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SEQUENCE FROM N.A.
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Q9KH15;
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                                                                                                                                                                                                                                                     108 DNSSSTTQNLNEAKTRLETAIRTAATSKQTFDEQHAELVKVYKELKTTLSNETATLAPYA 167
                                                                                                                                                                                                                              9 DANPINGO-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE-93162830; PubMed-8432610;
MARKham P.F., Glew M.D., Whithear K.G., Walker I.D.;
MACCOLLar cloning of a member of the gene family that encodes )
hemagglutnin of Mycoplasma gallisepticum.";
Infect. Immun. 61:903-909(1993).
EMBL; M33178; AAA02996.1; -.
EMBL; S55216; AAB25397.2; -.
                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.6%; Score 713; DB 2; Length 647;
11arity 41.1%; Pred. No. 2.5e-27;
Conservative 60; Mismatches 124; Indels
                                                                                                                                                                                   Indels
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MW; 33916673BB9E28C4 CRC64;
                                                               POTENTIAL.
356554BD2C72C1F8 CRC64;
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1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2700 (TrEMBLrel. 13, Last annotation update)
HEMAGGUTININ HOMOLOG PRECURSOR.
                                                                                                                                           37.1%; Score 743; DB 2;
42.3%; Pred. No. 8.8e-29;
tive 62; Mismatches 125;
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                                                               25 PC
70205 MW;
FEBS Lett. 352:347-352(1994).
EMBL: L28424; AAA62416.1; -.
Signal.
SIGNAL.
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NCBI_TaxID=2096;
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70333 N
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Best Local Similarity
Matches 172; Conserv
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647 A
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01-NOV-1996 (T
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Best Local Si
Matches 1699
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SEQUENCE
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228 NYKYARRTVWNGDEPSSRILANTNS-----ITDVSWIYSLAGTNTKYQFSFSNYGPS 279
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                                                                                                             DAQYAGIKMHLSGLYDAGKAITTKTLEPVEGDP-LTASAVMMANTKIVEAIKDEVLNPQK 226
                                                                                                                                                                                                                                                                                          TN----ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV----- 227
                                                                                                                                                                                                                                                                                                                        STGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSA----NNTTANPTPAVDE 333
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242 NNADQFANYQSFTLDKTKLENVEDA-----KKMGQPANYSFVGYSVDVTGTSGQETTIP
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                                                                                                                                                                                       STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK
                                                                                                                                                                                                                                                                                                                                                                                                  NYKYARRTVW-NGDEPSSRILANT-----NSITDVSWIYSLAGINTKYQFSFSNYGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shen Q.C., Bi D.R., Weng C.J.;
"Sequence analysis of the pMGA multigene family of Mycoplasma gallisepticum strain HS.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275312; AAF91413.1; -
SEQUENCE 656 AA: 70875 MW; 58EA7E075FC617E1 CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
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Last annotation update)
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Search completed: June 12, 2002, 10:50:42 Job time: 205 sec
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VRLTGLAFGKNT 419
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TGYLYFPYKLVKAADANNVGLQYKLN-NGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
                                           :|||||||||:
320 PQGVEPAQQQGDSSPKQASETQEVSPTPAAEVQAQQADTEQPATSQGTPLTDVSWIYSLS 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 NEHPNLVEAYKALKTTLEQR-ATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 GTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 CTSATIPTLNPTPNPEPKPDPMPNPPSGGMNGGNTNPGMDTAAQELASAKAALTTLTNRE 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 QPSNYSFVAFSADVTPV-----NYKYARRTVWNGDEPSSRILANTNS------
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: 090714; AAB50154.1; -
InterPro; IFR002819; HD
SEQUENCE 703 AA; 75742 MW; 310B69BE9F73CBC5 CRC64;
                                                                          339 IVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADK 383
                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                        703 A.A.
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01-DEC-2001 (TrEMBLrel.
HAEMAGGLUTININ.
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Best Local Similarity
Matches 167; Conserv
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STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLS--TINEQK 179
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                              --GPAASVDNINVAKVNLANLNFGENTIEFSVP-----MNKVAPMIGNMYITSDVAN 485
324 TANPIPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENN
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                                                                                                                                                                                                                                                        01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2000 (TrEMBLrel. 15, Last annotation update)
PMGA-LIKE PROTEIN 9.3 (FRAGMENT).
Mycoplasma qallisepticum.
Mycoplasma qallisepticum.
Mycoplasma yellisepticum.
Mycoplasma group; Mollicutes;
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF120770; AFF29525.1; -.
NON.TER 419 419
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